

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 23, 2005, 12:39:59 ; Search time 51.1475 Seconds  
(without alignments)  
300.354 Million cell updates/sec

Title: US-10-727-514-4

Perfect score: 147

Sequence: 1 APTSSSTKKTQLQLEHLLLDLQMLINGINN 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Uniprot\_03.\*

1: uniprot\_spport.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	147	100.0	150	2 Q9C001	homo sapien
2	147	100.0	153	1 IL2 HUMAN	P60568 homo sapien
3	147	100.0	153	1 IL2 HYLLA	P60569 hylobates l
4	147	100.0	153	2 Q6NZ93	P60293 homo sapien
5	147	100.0	154	1 IL2 MACFA	Q29615 macaca fasc
6	147	100.0	154	1 IL2 MACMU	P68291 macaca mula
7	147	100.0	154	1 IL2 MACNE	P68290 macaca neme
8	147	100.0	154	1 IL2 PAPAN	Q86591 papio anubi
9	145	98.6	154	1 IL2 SAISC	Q8mkh2 saimiri sci
10	145	98.6	154	2 Q7JFM2	Q7jfm2 aotus lemur
11	145	98.6	154	2 Q7JFM3	Q7jfm3 aotus nigri
12	145	98.6	154	2 Q7JFM4	Q7jfm4 aotus vocif
13	145	98.6	154	2 Q7JFM5	Q7jfm5 aotus nancy
14	145	98.6	154	2 Q9XS38	Q9xs38 papio hamad
15	143	97.3	133	2 Q6QWN0	Q6qwn0 homo sapien
16	143	97.3	133	2 Q7Z7M3	Q7z7m3 homo sapien
17	142	96.6	154	1 IL2 CERTO	P46649 cercopithec
18	137	93.2	153	2 Q6NZ91	Q6nz91 homo sapien
19	135.5	92.2	156	2 Q13169	Q13169 homo sapien
20	134	91.2	139	2 Q16334	Q16334 homo sapien
21	116	78.9	154	1 IL2 MIRAN	Q62641 mirounga an
22	114	77.6	154	1 IL2 FELCA	Q07885 felis silve
23	108.5	73.8	155	2 Q9XT83	Q9xt83 halichoerus
24	107.5	73.1	66	2 Q9BG74	Q9bg74 canis famil
25	107.5	73.1	155	1 IL2 CANFA	Q29416 canis famil
26	107	72.8	79	2 Q9TV12	Q9tv12 canis famil
27	107	72.8	152	2 Q80XG3	Q80xg3 peromyscus
28	107	72.8	153	1 IL2 RABIT	Q77620 oryctolagus
29	106	72.1	133	2 Q9MZR9	Q9mzr9 oryctolagus
30	106	72.1	155	2 Q923T2	Q923t2 sigmodon hi
31	103	70.1	138	2 Q70329	Q70329 mesocricetu

32	97	66.0	155	1	IL2 RAT	P17108 rattus norv
33	96	65.3	154	1	IL2 FIG	P26891 sus scrofa
34	95	64.6	155	1	IL2 MERUN	Q08081 meriones un
35	93	63.3	154	2	Q865X2	Q865x2 lama glama
36	92	62.6	149	1	IL2 HORSE	P37997 equus cabal
37	91	61.9	123	2	Q9UCFS	Q9ucfs homo sapien
38	88	59.9	152	1	IL2 ORCOR	Q97513 orcinus orc
39	87	59.2	38	2	Q71V48	Q71v48 homo sapien
40	83	56.5	154	2	Q9XT84	Q9xt84 delphinapte
41	82	55.8	152	2	Q88210	Q88210 cavia porce
42	79	53.7	69	2	Q9GJRA	Q9gjr4 ovia aries
43	79	53.7	136	2	Q8E220	Q8e220 capra hircu
44	79	53.7	145	2	Q8HZ67	Q8hz67 bos indicu
45	79	53.7	155	1	IL2 BOVIN	Q05016 bos taurus
46	79	53.7	155	1	IL2 BUBBU	P95kp3 bubalus bub
47	79	53.7	155	1	IL2_CAPHI	P36835 capra hircu
48	79	53.7	155	1	IL2_SHEEP	P19114 ovies aries
49	79	53.7	155	2	Q8HYR7	Q8hyr7 bos taurus
50	79	53.7	155	2	Q9GL83	Q9gl83 capra hircu
51	79	53.7	162	1	IL2 CEREL	P51747 cervus elap
52	77	52.4	147	2	Q7YRQ2	Q7yrq2 bos mutus g
53	69	46.9	39	2	Q9BG73	Q9bg73 canis famil
54	69	46.9	150	2	P70291	P70291 mus musculu
55	69	46.9	169	2	Q9QUS8	Q9qus8 mus musculu
56	67	45.6	150	2	P70294	P70294 mus musculu
57	64.5	43.9	166	1	IL2 MUSSP	Q08867 mus spretus
58	64	43.5	63	2	Q8BHA4	Q8bha4 mus musculu
59	64	43.5	169	1	IL2 MOUSE	P04351 mus musculu
60	62.5	42.5	159	2	P70293	P70293 mus musculu
61	60.5	41.2	155	2	P70292	P70292 mus musculu
62	59	40.1	155	2	Q85QE7	Q85qe7 manheimia
63	54	36.7	357	1	AAAA_EMENT	P21133 emeritella
64	52	35.4	101	2	Q6DUY6	Q6duy6 cryptospori
65	52	35.4	116	2	Q29138	Q29138 trichechus
66	52	35.4	285	2	Q83F57	Q83f57 coxiella bu
67	52	35.4	300	2	Q8VW37	Q8vw37 coxiella bu
68	52	35.4	300	2	Q841J1	Q841j1 coxiella bu
69	52	35.4	304	2	Q841J2	Q841j2 coxiella bu
70	52	35.4	304	2	Q841X8	Q841x8 campylobact
71	52	35.4	737	2	Q9KTG5	Q9ktg5 vibrio chol
72	52	35.4	1530	2	Q81BS2	Q81bs2 plasmodium
73	51.5	35.0	2673	2	Q7QPT6	Q7qpt6 giardia lam
74	51	34.7	95	2	Q8BN23	Q8bn23 mus musculu
75	51	34.7	304	2	Q930K5	Q930k5 rhizobium m
76	51	34.7	457	2	Q9NIP5	Q9nip5 strongyloce
77	51	34.7	517	2	Q8R6R8	Q8r6r8 thermoplaea
78	51	34.7	627	1	FLGK_BORBU	P70859 borrelia bu
79	51	34.7	627	2	Q86213	Q862i3 borrelia ga
80	51	34.7	746	2	Q6FNH5	Q6fnh5 candida gla
81	50	34.0	365	2	P71599	P71599 mycobacteri
82	50	34.0	365	2	Q7U2Z7	Q7u2z7 mycobacteri
83	50	34.0	1046	1	POL_SIVAG	P27980 simian immu
84	50	34.0	1454	1	CSP2_HUMAN	O60244 h cofactor
85	50	34.0	3175	1	RPOA_EAV	P19811 equine arte
86	49.5	33.7	715	2	Q8EJ30	Q8ej30 shewanella
87	49.5	33.7	1518	2	Q7RA10	Q7ra10 plasmodium
88	49	33.3	104	2	Q632T6	Q632t6 bacillus th
89	49	33.3	104	2	Q6HCC6	Q6hcc6 bacillus th
90	49	33.3	149	2	Q7R1Q4	Q7rlq4 giardia lam
91	49	33.3	262	2	Q75ZP3	Q75zp3 sus scrofa
92	49	33.3	315	2	Q6L2K3	Q6l2k3 picophorus
93	49	33.3	322	2	Q72UY1	Q72uy1 leptospira
94	49	33.3	322	2	Q8E2Z2	Q8e2z2 leptospira
95	49	33.3	334	2	Q7NRQ8	Q7nrq8 chromobacte
96	49	33.3	456	2	Q6BS49	Q6bs49 debaryomyce
97	49	33.3	458	2	O15996	O15996 hemimentrot
98	49	33.3	543	2	Q9KSF8	Q9ksf8 vibrio chol
99	49	33.3	602	2	Q8DYP7	Q8dyp7 streptococc
100	49	33.3	602	2	Q8E4A4	Q8e4a4 streptococc

ALIGNMENTS

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RESULT 1
ID Q9C001 PRELIMINARY; PRT; 150 AA.
AC Q9C001;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interleukin-2 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=20345237; PubMed=11093171;
RX DOI=10.1002/1521-4141(200012)30:12<3516::AID-IMMU3516>3.0.CO;2-S;
RA Matesanz F., Delgado C., Fresno M., Alcina A.;
RT "Allelic selection of human IL-2 gene.";
RL Eur. J. Immunol. 30:3516-3521(2000).
DR EMBL; AF228636; AAG53575.1; -.
DR HSSP; P60568; IIRL.
DR GO; GO:0005576; C:cytoplasmic; IEA.
DR GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PD00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
DR NON_TER 150 150
FT SEQUENCE 150 AA; 17312 MW; BF25860F8436ACE5 CRC64;

Query Match 100.0%; Score 147; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 5,1e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLQLHLLLDLQMLINGNN 30
Db 21 APTSSSTKKTQLQLHLLLDLQMLINGNN 50

RESULT 2
ID IL2_HUMAN STANDARD; PRT; 153 AA.
AC P60568; P01585;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF)
DE (Aldeleukin).
GN Name=IL2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=84247353; PubMed=6330695;
RA Holbrook N.J., Lieber M., Crabtree G.R.;
RT "DNA sequence of the 5' flanking region of the human interleukin 2 gene: homologues with adult T-cell leukemia virus.";
RL Nucleic Acids Res. 12:5005-5013(1984).
RN [2]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=83167472; PubMed=6403867;
RA Taniguchi T., Maecu H., Fujita T., Takaoka C., Kashima N.,
RA Yoshimoto R., Hamuro J.;
RT "Structure and expression of a cloned cDNA for human interleukin-2.";
RL Nature 302:305-310(1983).
RN [3]_TaxID=9606;

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RP SEQUENCE FROM N.A.
RX MEDLINE=84023840; PubMed=6312994;
RA Maeda S., Nishino N., Obaru K., Mita S., Nomiya H., Shimada K.,
RA Fujimoto K., Teranishi T., Hirano T., Onoue K.;
RT "Cloning of interleukin 2 mRNAs from human tonsils.";
RL Biochem. Biophys. Res. Commun. 115:1040-1047(1983).
RN [4]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=83246551; PubMed=6306584;
RA Devos R., Plaetnick G., Cheroutre H., Simons G., Degraeve W.,
RA Tavernier J., Remaut E., Fiers W.;
RT "Molecular cloning of human interleukin 2 cDNA and its expression in E. coli.";
RL Nucleic Acids Res. 11:4307-4323(1983).
RN [5]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=84170356; PubMed=6608729;
RA Holbrook N.J., Smith K.A., Fornace A.J. Jr., Comeau C.M.,
RA Wiskocil R.L., Crabtree G.R.;
RT "T-cell growth factor: complete nucleotide sequence and organization of the gene in normal and malignant cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:1634-1638(1984).
RN [6]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=84170243; PubMed=6324170;
RA Fujita T., Takaoka C., Matsui H., Taniguchi T.;
RT "Structure of the human interleukin 2 gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:7437-7441(1983).
RN [7]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=95239150; PubMed=7722480;
RA Eisenberg O., Faber-Elman A., Lotan M., Schwartz M.;
RT "Interleukin-2 transcripts in human and rodent brains: possible expression by astrocytes.";
RL J. Neurochem. 64:1928-1936(1995).
RN [8]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=96422299; PubMed=8824916;
RX DOI=10.1002/(SICI)1098-2795(199602)43:2<180::AID-MRD7>3.3.CO;2-D;
RA Chernicky C.L., Tan H., Burfeind P., Ilan J., Ilan J.;
RT "Sequence of interleukin-2 isolated from human placental poly A+ RNA: possible role in maintenance of fetal allograft.";
RL Mol. Reprod. Dev. 43:180-186(1996).
RN [9]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen J.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

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CC -----
DR EMBL; M11144; AAA35454.1; -.
DR PIR; A94067; ICGI2
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN 2; 1.
DR PROSITE; PS00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN 2; 1.
KW Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
FT SIGNAL 1 20 By similarity.
FT CHAIN 21 153 Interleukin-2.
FT CARBOHYD 23 23 O-linked (GalNAc. . .) (By similarity).
FT DISULFID 78 125 By similarity.
SQ SEQUENCE 153 AA; 17628 MW; 59E2F40F25860F84 CRC64;

Query Match 100.0%; Score 147; DB 1; Length 153;
Best Local Similarity 100.0%; Pred. No. 5.2e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLLDLQMLNGINN 30
DB 21 APTSSSTKKTQLEHLLLDLQMLNGINN 50

RESULT 4
Q6N293 PRELIMINARY; PRT; 153 AA.
ID Q6N293
AC Q6N293
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Interleukin 2.
GN Name=IL2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buecaw K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RA Strausberg R.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC066254; AAH66254.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.

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DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN 2; 1.
SQ SEQUENCE 153 AA; 17597 MW; 1942F50F25960E88 CRC64;

Query Match 100.0%; Score 147; DB 2; Length 153;
Best Local Similarity 100.0%; Pred. No. 5.2e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLLDLQMLNGINN 30
DB 21 APTSSSTKKTQLEHLLLDLQMLNGINN 50

RESULT 5
IL2_MACFA STANDARD; PRT; 154 AA.
ID IL2_MACFA
AC Q29615;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN Name=IL2;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA Yabe M., Matsumura Y., Tatsumi M.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Produced by T-cells in response to antigenic or
CC mitogenic stimulation, this protein is required for T-cell
CC proliferation and other activities crucial to regulation of the
CC immune response. Can stimulate B cells, monocytes, lymphokine-
CC activated killer cells, natural killer cells, and glioma cells (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-2 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D63352; BAA09676.1; -.
DR HSP; P01585; IMA9.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN 2; 1.
KW Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
FT SIGNAL 1 20 By similarity.
FT CHAIN 21 154 Interleukin-2.
FT CARBOHYD 23 23 O-linked (GalNAc. . .) (By similarity).
FT DISULFID 78 126 By similarity.
SQ SEQUENCE 154 AA; 17686 MW; 7853FE624A5E4A49 CRC64;

Query Match 100.0%; Score 147; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 5.2e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 APTSSSTKKTQLQLEHLLDLQMLNGINN 30
      |||
      21 APTSSSTKKTQLQLEHLLDLQMLNGINN 50
      |||

RESULT 6
IL2_MACMU
ID IL2_MACMU STANDARD; PRT; 154 AA.
AC P68291; P51498;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN Name=IL2;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
nonhuman primates.";
RL J. Immunol. 155:3946-3954 (1995).
CC -!- FUNCTION: Produced by T-cells in response to antigenic or
CC mitogenic stimulation, this protein is required for T-cell
CC proliferation and other activities crucial to regulation of the
CC immune response. Can stimulate B cells, monocytes, lymphokine-
CC activated killer cells, natural killer cells, and glioma cells (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-2 family.
CC
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CC
CC EMBL; U19847; AAB60400.1; -.
CC HSPG; P01585; I448.
CC InterPro; IPR009079; 4_helix_cytokine.
CC InterPro; IPR000779; Interleukin-2.
CC Pfam; PF00715; IL2; 1.
CC PRINTS; PR00265; INTERLEUKIN2.
CC SMART; SM00189; IL2; 1.
CC PROSITE; PS00424; INTERLEUKIN_2; 1.
CC Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
CC T-cell.
CC SIGNAL 1 20 By similarity.
CC CHAIN 21 154 Interleukin-2.
CC CARBOHYD 23 23 O-linked (GalNAc...) (By similarity).
CC DISULFID 78 126 By similarity.
CC SEQUENCE 154 AA; 17685 MW; 6AEB480F204BA49 CRC64;

Query Match 100.0%; Score 147; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 5.2e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 APTSSSTKKTQLQLEHLLDLQMLNGINN 30
      |||
      21 APTSSSTKKTQLQLEHLLDLQMLNGINN 50
      |||

RESULT 7
IL2_MACNE
ID IL2_MACNE STANDARD; PRT; 154 AA.
AC P68291; P51498;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN Name=IL2;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
nonhuman primates.";
RL J. Immunol. 155:3946-3954 (1995).
CC -!- FUNCTION: Produced by T-cells in response to antigenic or
CC mitogenic stimulation, this protein is required for T-cell
CC proliferation and other activities crucial to regulation of the
CC immune response. Can stimulate B cells, monocytes, lymphokine-
CC activated killer cells, natural killer cells, and glioma cells (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-2 family.
CC
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CC
CC EMBL; U19847; AAB60400.1; -.
CC HSPG; P01585; I448.
CC InterPro; IPR009079; 4_helix_cytokine.
CC InterPro; IPR000779; Interleukin-2.
CC Pfam; PF00715; IL2; 1.
CC PRINTS; PR00265; INTERLEUKIN2.
CC SMART; SM00189; IL2; 1.
CC PROSITE; PS00424; INTERLEUKIN_2; 1.
CC Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
CC T-cell.
CC SIGNAL 1 20 By similarity.
CC CHAIN 21 154 Interleukin-2.
CC CARBOHYD 23 23 O-linked (GalNAc...) (By similarity).
CC DISULFID 78 126 By similarity.
CC SEQUENCE 154 AA; 17685 MW; 6AEB480F204BA49 CRC64;

Query Match 100.0%; Score 147; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 5.2e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 APTSSSTKKTQLQLEHLLDLQMLNGINN 30
      |||
      21 APTSSSTKKTQLQLEHLLDLQMLNGINN 50
      |||

RESULT 8
IL2_PAPAN
ID IL2_PAPAN STANDARD; PRT; 154 AA.
AC Q865Y1;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN Name=Il2; Synonyms=Il-2;
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;

```

OC Cercopithecinae; Papio.  
 OX NCBI\_TaxID=9555;  
 RN [1]\_SIMILARITY: Belongs to the IL-2 family.  
 RP SEQUENCE FROM N.A.  
 RA Villinger F.;  
 RT "Nonhuman primate cytokines.";  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Produced by T-cells in response to antigenic or  
 CC mitogenic stimulation, this protein is required for T-cell  
 CC proliferation and other activities crucial to regulation of the  
 CC immune response. Can stimulate B cells, monocytes, lymphokine-  
 CC activated killer cells, natural killer cells, and glioma cells (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the IL-2 family.  
 CC  
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 CC  
 CC EMBL; AY234220; AA085333.1; -.  
 CC HSSP; P01585; IMA9.  
 DR InterPro; IPR009079; 4\_helix\_cytokine.  
 DR InterPro; IPR000779; Interleukin-2.  
 DR Pfam; PF00715; IL2; 1.  
 DR PRINTS; PR00265; INTERLEUKIN2.  
 DR ProDom; PD003649; Interleukin-2; 1.  
 DR SMART; SM00189; IL2; 1.  
 DR PROSITE; PS00424; INTERLEUKIN 2; 1.  
 KW Cytokine; Glycoprotein; Growth factor; Immune response; Signal;  
 FT SIGNAL 1 20 By similarity.  
 FT CHAIN 21 154 Interleukin-2.  
 FT DISULFID 78 126 By similarity.  
 FT CARBOHYD 23 23 O-linked (GalNAc...) (By similarity).  
 SQ SEQUENCE 154 AA; 17713 MW; 47F48BDF204AD6E CRC64;  
 Query Match 100.0%; Score 147; DB 1; Length 154;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-14;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 APTSSSTKKTQLEHLLLDQMILNGINN 30  
 DB 21 APTSSSTKKTQLEHLLLDQMILNGINN 50  
 RESULT 9  
 IL2\_SAISC  
 ID IL2\_SAISC STANDARD; PRT; 154 AA.  
 AC Q8MKH2;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).  
 GN Name=IL2;  
 OS Saimiri sciureus (Common squirrel monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.  
 OX NCBI\_TaxID=9521;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21972723; PubMed=11976788; DOI=10.1007/s00251-002-0443-y;  
 RA Heraud J.M., Laverne A., Kazanji M.;  
 RT "Molecular cloning, characterization, and quantification of squirrel  
 RT monkey (Saimiri sciureus) Th1 and Th2 cytokines.";  
 RL Immunogenetics 54:20-29(2002).  
 CC -!- FUNCTION: Produced by T-cells in response to antigenic or  
 CC mitogenic stimulation, this protein is required for T-cell  
 CC proliferation and other activities crucial to regulation of the

CC immune response. Can stimulate B cells, monocytes, lymphokine-  
 CC activated killer cells, natural killer cells, and glioma cells (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the IL-2 family.  
 CC  
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 CC  
 CC EMBL; AF294755; AA032042.1; -.  
 CC HSSP; P01585; IMA9.  
 DR InterPro; IPR009079; 4\_helix\_cytokine.  
 DR InterPro; IPR000779; Interleukin-2.  
 DR Pfam; PF00715; IL2; 1.  
 DR PRINTS; PR00265; INTERLEUKIN2.  
 DR ProDom; PD003649; Interleukin-2; 1.  
 DR SMART; SM00189; IL2; 1.  
 DR PROSITE; PS00424; INTERLEUKIN 2; 1.  
 KW Cytokine; Glycoprotein; Growth factor; Immune response; Signal;  
 FT SIGNAL 1 20 By similarity.  
 FT CHAIN 21 154 Interleukin-2.  
 FT DISULFID 78 126 By similarity.  
 FT CARBOHYD 23 23 O-linked (GalNAc...) (By similarity).  
 SQ SEQUENCE 154 AA; 17657 MW; AA642BABBCA87569 CRC64;  
 Query Match 98.6%; Score 145; DB 1; Length 154;  
 Best Local Similarity 96.7%; Pred. No. 1e-13;  
 Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 APTSSSTKKTQLEHLLLDQMILNGINN 30  
 DB 21 APTSSSTKKTQLEHLLLDQMILNGINN 50  
 RESULT 10  
 O7JFM2  
 ID O7JFM2 PRELIMINARY; PRT; 154 AA.  
 AC O7JFM2;  
 DT 05-JUL-2004 (TReMBLrel. 27, Created)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
 DE IL-2.  
 OS Aotus lemurinus (Northern gray-necked night monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotus.  
 OX NCBI\_TaxID=43147;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A.,  
 RA Patarroyo M.E.;  
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U88364; AAD41534.1; -.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005134; F:interleukin-2 receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR009079; 4\_helix\_cytokine.  
 DR InterPro; IPR000779; Interleukin-2.  
 DR Pfam; PF00715; IL2; 1.  
 DR PRINTS; PR00265; INTERLEUKIN2.  
 DR ProDom; PD003649; Interleukin-2; 1.  
 DR SMART; SM00189; IL2; 1.  
 DR PROSITE; PS00424; INTERLEUKIN 2; 1.  
 SQ SEQUENCE 154 AA; 17675 MW; AB752ABBADA96469 CRC64;  
 Query Match 98.6%; Score 145; DB 2; Length 154;  
 Best Local Similarity 96.7%; Pred. No. 1e-13;  
 Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 APTSSSTKKTQLEHLLLDLQMLNGINN 30
Db 21 APTSSSTKKTQLEHLLLDLQMLNGINN 50

RESULT 11
Q7JFM3
ID Q7JFM3 PRELIMINARY; PRT; 154 AA.
AC Q7JFM3;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE IL-2.
OS Aotus nigriceps (Black-headed owl monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57175;
RN [1]
RP SEQUENCE FROM N.A.
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A.,
RA Patarroyo M.E.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88363; AAD41536.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005134; P:interleukin-2 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 154 AA; 17675 MW; AB752ABBADA96469 CRC64;

Query Match 98.6%; Score 145; DB 2; Length 154;
Best Local Similarity 96.7%; Pred. No. 1e-13;
Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLLDLQMLNGINN 30
Db 21 APTSSSTKKTQLEHLLLDLQMLNGINN 50

RESULT 12
Q7JFM4
ID Q7JFM4 PRELIMINARY; PRT; 154 AA.
AC Q7JFM4;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE IL-2.
OS Aotus vociferans (Spix's owl monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57176;
RN [1]
RP SEQUENCE FROM N.A.
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A.,
RA Patarroyo M.E.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88362; AAD41537.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005134; P:interleukin-2 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 154 AA; 17675 MW; AB752ABBADA96469 CRC64;

Query Match 98.6%; Score 145; DB 2; Length 154;
Best Local Similarity 96.7%; Pred. No. 1e-13;
Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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SQ SEQUENCE 154 AA; 17675 MW; AB752ABBADA96469 CRC64;

Query Match 98.6%; Score 145; DB 2; Length 154;
Best Local Similarity 96.7%; Pred. No. 1e-13;
Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLLDLQMLNGINN 30
Db 21 APTSSSTKKTQLEHLLLDLQMLNGINN 50

RESULT 13
Q7JFM5
ID Q7JFM5 PRELIMINARY; PRT; 154 AA.
AC Q7JFM5;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE IL-2.
OS Aotus nancymae (Ma's night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=37293;
RN [1]
RP SEQUENCE FROM N.A.
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A.,
RA Patarroyo M.E.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88361; AAD41535.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005134; P:interleukin-2 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 154 AA; 17675 MW; AB752ABBADA96469 CRC64;

Query Match 98.6%; Score 145; DB 2; Length 154;
Best Local Similarity 96.7%; Pred. No. 1e-13;
Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLLDLQMLNGINN 30
Db 21 APTSSSTKKTQLEHLLLDLQMLNGINN 50

RESULT 14
Q9XS38
ID Q9XS38 PRELIMINARY; PRT; 154 AA.
AC Q9XS38;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE IL-2.
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Papio.
OX NCBI_TaxID=9557;
RN [1]
RP SEQUENCE FROM N.A.
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A.,
RA Patarroyo M.E.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88365; AAD41538.1; -.
DR HSP; P60568; IIRL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005134; P:interleukin-2 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.

```

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DR InterPro; IPR009079; 4_helix cytokine.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00285; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN 2; 1.
SQ SEQUENCE 154 AA; 17675 MW; AB752ABBADA96469 CRC64;

Query Match 98.6%; Score 145; DB 2; Length 154;
Best Local Similarity 96.7%; Pred. No. 1e-13;
Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSSSTKTKTQLQLEHLLDLQMLNGINN 30
DB 21 APTSSSTKTKTQLQLEHLLDLQMLNGINN 50

RESULT 15
Q6QWN0 PRELIMINARY; PRT; 133 AA.
ID Q6QWN0
AC Q6QWN0;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Interleukin-2
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Chikara S.K., Sharma G.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY232040; AAS17753.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00285; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN 2; 1.
SQ SEQUENCE 133 AA; 15462 MW; 1699F680A09DB3B0 CRC64;

Query Match 97.3%; Score 143; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.8e-13;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PTSSSTKTKTQLQLEHLLDLQMLNGINN 30
DB 2 PTSSSTKTKTQLQLEHLLDLQMLNGINN 30

RESULT 16
Q7Z7M3 PRELIMINARY; PRT; 133 AA.
ID Q7Z7M3
AC Q7Z7M3;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Interleukin-2
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Chikara S.K., Jaiswal P., Sharma G.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY283686; AAP35033.1; -.

DR InterPro; IPR009079; 4_helix cytokine.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00285; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN 2; 1.
SQ SEQUENCE 133 AA; 15461 MW; 1699FEA880959B90 CRC64;

Query Match 97.3%; Score 143; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.8e-13;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 PTSSSTKTKTQLQLEHLLDLQMLNGINN 30
DB 2 PTSSSTKTKTQLQLEHLLDLQMLNGINN 30

RESULT 17
IL2 CERTO
ID IL2 CERTO STANDARD; PRT; 154 AA.
AC P45649;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN Name=IL2;
OS Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Cercocebus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and nonhuman primates.";
RL J. Immunol. 155:3946-3954 (1995).
CC -!- FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokine-activated killer cells, natural killer cells, and glioma cells.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-2 family.

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EMBL; U19846; AAB60399.1; -.
HSSP; P01585; IM47.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00285; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN 2; 1.
KW Cytokine; Glycoprotein; Growth factor; Immune response; Signal; T-cell.
FT SIGNAL 1 20 By similarity.
FT CHAIN 21 154 Interleukin-2.
FT CARBOHYD 23 23 O-linked (GalNAc...) (By similarity).
```



FT DISULFID 78 126 By similarity.  
 FT VARIANT 25 25 R -> S.  
 FT VARIANT 74 74 K -> E.  
 SQ SEQUENCE 154 AA; 17754 MW; 9FBE51814204BA48 CRC64;

Query Match 96.6%; Score 142; DB 1; Length 154;  
 Best Local Similarity 96.7%; Pred. No. 3e-13;  
 Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKTQLEHLLDLQMLNGINN 30  
 |||||  
 Db 21 APTSSSTKTQLEHLLDLQMLNGINN 50

## RESULT 18

Q6NZ91 PRELIMINARY; PRT; 153 AA.  
 AC Q6NZ91;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DE Interleukin 2.  
 GN Name=IL2;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PCR rescued clones;  
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska J., Smalusz D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PCR rescued clones;  
 RA Strausberg R.;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC066256; AAH66256.1; -;  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005134; F:interleukin-2 receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR009079; 4 helix cytokine.  
 DR InterPro; IPR00779; Interleukin-2.  
 DR Pfam; PF00715; IL2; 1.  
 DR PRINTS; PR00265; INTERLEUKIN2.  
 DR ProDom; PD003649; Interleukin-2; 1.  
 DR SMART; SM00189; IL2; 1.  
 DR PROSITE; PS00424; INTERLEUKIN 2; 1.  
 SQ SEQUENCE 153 AA; 17644 MW; 59F9980409964F84 CRC64;

Query Match 93.2%; Score 137; DB 2; Length 153;  
 Best Local Similarity 96.7%; Pred. No. 1.7e-12;  
 Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 APTSSSTKTQLEHLLDLQMLNGINN 30  
 |||||  
 Db 21 ALTSSSTKTQLEHLLDLQMLNGINN 50

## RESULT 19

Q13169 PRELIMINARY; PRT; 156 AA.  
 AC Q13169;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Interleukin 2.  
 GN Name=IL2;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Xu D., Wu Y., Chen J., Yu L., Zhong M., Hui Y., Qu H.;  
 RT "Expression of human IL-2 from gene transferred mouse melanoma cells  
 and its effect on the growth of mouse melanoma."  
 RL Chin. J. Microbiol. Immunol. 13:78-82(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Xu L.;  
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U25676; AAA70092.1; -;  
 DR HSSP; P60568; IIRL.  
 DR GO; GO:0005576; C:extracellular; TAS.  
 DR GO; GO:0005134; F:interleukin-2 receptor binding; TAS.  
 DR GO; GO:0019209; P:kinase activator activity; TAS.  
 DR GO; GO:0006916; P:anti-apoptosis; TAS.  
 DR GO; GO:0007267; P:cell-cell signaling; TAS.  
 DR GO; GO:0006955; P:immune response; TAS.  
 DR GO; GO:0030101; P:natural killer cell activation; TAS.  
 DR GO; GO:0030307; P:positive regulation of cell growth; TAS.  
 DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.  
 DR GO; GO:0030217; P:T-cell differentiation; TAS.  
 DR InterPro; IPR009079; 4 helix cytokine.  
 DR InterPro; IPR00779; Interleukin-2.  
 DR Pfam; PF00715; IL2; 1.  
 DR PRINTS; PR00265; INTERLEUKIN2.  
 DR ProDom; PD003649; Interleukin-2; 1.  
 DR SMART; SM00189; IL2; 1.  
 DR PROSITE; PS00424; INTERLEUKIN 2; 1.  
 SQ SEQUENCE 156 AA; 18002 MW; 8E0452D43B336389 CRC64;

Query Match 92.2%; Score 135.5; DB 2; Length 156;  
 Best Local Similarity 90.9%; Pred. No. 2.9e-12;  
 Matches 30; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 APTSSSTKTQLEHLLDLQMLNGINN 30  
 |||||  
 Db 21 APTSSSTKTQLEHLLDLQMLNGINN 53

## RESULT 20

Q16334 PRELIMINARY; PRT; 139 AA.  
 AC Q16334;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE IL-2 protein (Fragment).  
 GN Name=IL-2;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.

```

RX MEDLINE=95239150; PubMed=7722480;
RA Bizenberg O., Faber-Elman A., Lotan M., Schwartz M.;
RT "Interleukin-2 transcripts in human and rodent brains: possible
expression by astrocytes.";
RL J. Neurochem. 64:1928-1936(1995).
DR EMBL; S77835; AAD14264.1; -.
DR HSSP; P60568; IIRL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0003134; F:interleukin-2 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
FT NON_TER 139
FT SEQUENCE 139 AA; 15986 MW; 731FBA406D0C63C5 CRC64;

Query Match 91.2%; Score 134; DB 2; Length 139;
Best Local Similarity 93.3%; Pred. No. 4.3e-12;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 APTSSSTKTKTQLQLHLLLDLQMLGNN 30
||||| 17 APTSSSTKTKTQLXLEHLLLDLQMLXGNN 46
Db

RESULT 21
IL2_MIRAN
ID IL2_MIRAN STANDARD; PRT; 154 AA.
AC O62641;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN Name=IL2;
OS Mirounga angustirostris (Northern elephant seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Mirounga.
OX NCBI_TaxID=9716;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98136706; PubMed=9476229;
RA Shoda L.K.M., Brown W.C., Rice-Ficht A.C.;
RT "Sequence and characterization of phocine interleukin 2.";
RL J. Wildl. Dis. 34:81-90(1998).
CC -!- FUNCTION: Produced by T-cells in response to antigenic or
CC mitogenic stimulation, this protein is required for T-cell
CC proliferation and other activities crucial to regulation of the
CC immune response. Can stimulate B cells, monocytes, lymphokine-
CC activated killer cells, natural killer cells, and glioma cells (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-2 family.
CC
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CC
CC EMBL; U79187; AAC12258.1; -.
CC HSSP; P01585; 1M49.
CC InterPro; IPR009079; 4 helix cytokine.
CC InterPro; IPR000779; Interleukin-2.
CC Pfam; PF00715; IL2; 1.
CC PRINTS; PR00265; INTERLEUKIN2.
CC ProDom; PD003649; Interleukin-2; 1.
CC SMART; SM00189; IL2; 1.

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DR PROSITE; PS00424; INTERLEUKIN_2; 1.
KW Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
FT T-cell.
FT SIGNAL 1 20 By similarity.
FT CHAIN 21 154 Interleukin-2.
FT CARBOHYD 23 23 O-linked (Galnac. .) (By similarity).
FT DISULFID 78 126 By similarity.
SQ SEQUENCE 154 AA; 17661 MW; 0C92337A4B16B6B CRC64;

Query Match 78.9%; Score 116; DB 1; Length 154;
Best Local Similarity 73.3%; Pred. No. 2.6e-09;
Matches 22; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 1 APTSSSTKTKTQLQLHLLLDLQMLGNN 30
||||| 21 APTTSTKTQQLLEQLLDLRLLELNGVN 50
Db

RESULT 22
IL2_FELCA
ID IL2_FELCA STANDARD; PRT; 154 AA.
AC Q07885;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN Name=IL2;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93356765; PubMed=8352761;
RA Cozzi P.J., Padrid P.A., Takeda J., Alegre M.-A., Yuhki N., Leff A.R.;
RT "Sequence and functional characterization of feline interleukin 2.";
RL Biochem. Biophys. Res. Commun. 194:1038-1043(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Litman R., Gibbs C., Good R.A., Day N.K.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBSJ databases.
CC -!- FUNCTION: Produced by T-cells in response to antigenic or
CC mitogenic stimulation, this protein is required for T-cell
CC proliferation and other activities crucial to regulation of the
CC immune response. Can stimulate B cells, monocytes, lymphokine-
CC activated killer cells, natural killer cells, and glioma cells.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-2 family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L19402; AAA02865.1; -.
CC EMBL; L25408; AAA51431.1; -.
CC PIR; JN0698; JN0698.
CC HSSP; P01585; 1M49.
CC InterPro; IPR009079; 4 helix cytokine.
CC InterPro; IPR000779; Interleukin-2.
CC Pfam; PF00715; IL2; 1.
CC PRINTS; PR00265; INTERLEUKIN2.
CC ProDom; PD003649; Interleukin-2; 1.
CC SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
KW Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
FT T-cell.
FT SIGNAL 21 154 Interleukin-2.
FT CHAIN 21 154 By similarity.
FT DISULFID 78 126 By similarity.

```

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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
RL EMBL; AF333117; AAK01437.1; -.
DR HSSP; P60568; 11RL.
DR GO; GO:0005576; C:extracellular; IEA.
DR DR GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR000779; interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR PRODom; PD003649; interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR NON_TER 1
FT TER 66
SQ SEQUENCE 66 AA; 7389 MW; 22A893F79DA2AE47 CRC64;

Query Match 73.1%; Score 107.5; DB 2; Length
Best Local Similarity 71.0%; Pred. No. 1.9e-08;
Matches 22; Conservative 6; Mismatches 2; Indels

QY 1 AP-TSSSTKTKTQLQLEHLLDLQMLINGNN 30
||| ||||| : | : ||||| : ||| : |||
DB 14 APITSSSTKETEQMEQLLDLQLLINGVNN 44

RESULT 25
IL2_CANFA STANDARD; PRT; 155 AA.
AC Q29416; Q28249;
AD IL2_CANFA
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-2 precursor (IL-2) ('T-cell growth factor') (T
GN Name:IL2;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
OC Mammalia; Rutheria; Carnivora; Fissipedia; Canidae; Cani
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=XBRE21/12/93; TISSUE=Lymph node;
RX MEDLINE=95337423; PubMed=7612950;
RA Dunham S.P., Argyle D.J., Onions D.E.;
RT "The isolation and sequence of canine interleukin-2.";
RL DNA Seq. 5:177-180 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=96016696; PubMed=8571541; DOI=10.1016/0165-2427(
RX Somberg R.L., Pullen R.P., Casal M.L., Patterson D.F., F
RA Knapp D.W., Williams J.S., Andriani O.M.;
RT "Cloning of the canine interleukin-2-encoding cDNA.";
RL Gene 159:281-282 (1995).
RN [-] FUNCTION: Produced by T-cells in response to antigen
CC mitogenic stimulation. This protein is required for
CC proliferation and other activities crucial to regula
CC immune response. Can stimulate B cells, monocytes, i
CC activated killer cells, natural killer cells, and gl
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the IL-2 family.
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EMBL; D30710; BAA06378.1; -;  
 DR EMBL; U28141; AAA68969.1; -;  
 DR EMBL; U11689; AAA75360.1; -;  
 DR HSP; P01585; 3INK.  
 DR InterPro; IPR009079; 4\_helix\_cytokine.  
 DR InterPro; IPR000779; Interleukin-2.  
 DR Pfam; PF00715; IL2; 1.  
 DR PRINTS; PR00265; INTERLEUKIN2.  
 DR ProDom; PD003649; Interleukin-2; 1.  
 DR SMART; SM00189; IL2; 1.  
 DR PROSITE; PS00424; INTERLEUKIN\_2; 1.  
 KW Cytokine; Glycoprotein; Growth factor; Immune response; Signal;  
 FT SIGNAL. 1 20  
 FT CHAIN 21 155  
 FT CARBOHYD 24 24  
 FT CARBOHYD 112 112  
 FT DISULFID 79 127  
 FT CONFLICT 4 4  
 FT CONFLICT 37 37  
 FT CONFLICT 151 151  
 FT CONFLICT 154 154  
 FT CONFLICT 155 AA; 17668 MW; D13E486B7F4AC1D CRC64;  
 SQ SEQUENCE 155 AA; 17668 MW; D13E486B7F4AC1D CRC64;

Query Match 73.1%; Score 107.5; DB 1; Length 155;  
 Best Local Similarity 71.0%; Pred. No. 5.1e-08;  
 Matches 22; Conservative 6; Mismatches 2; Indels 1; Gaps 1;  
 QY 1 AP-TSSSTKKTQLEHLLDQLMILNGINN 30  
 DB 21 APTSSSTKETEQQMEQLLDQLLLGVNN 51

RESULT 26  
 Q9TV12 PRELIMINARY; PRT; 79 AA.  
 AC Q9TV12;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Interleukin-2 (Fragment).  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OC NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA German A.J., Helpe C.R., Harley R., Hall E.J., Day M.J.;  
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF091131; AAD46989.1; -;  
 DR HSP; P60568; 1IRL.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005134; F:interleukin-2 receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR009079; 4\_helix\_cytokine.  
 DR Pfam; PF00715; IL2; 1.  
 DR PRINTS; PR00265; INTERLEUKIN2.  
 DR ProDom; PD003649; Interleukin-2; 1.  
 DR SMART; SM00189; IL2; 1.  
 DR PROSITE; PS00424; INTERLEUKIN\_2; 1.  
 FT NON TER 1  
 FT NON TER 79  
 SQ SEQUENCE 79 AA; 9087 MW; 83079BF8FA659BD CRC64;

Query Match 72.8%; Score 107; DB 2; Length 79;  
 Best Local Similarity 71.4%; Pred. No. 2.8e-08;  
 Matches 20; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 3 TSSSTKKTQLEHLLDQLMILNGINN 30  
 DB 7 TSSSTKETEQQMEQLLDQLLLGVNN 34  
 RESULT 27  
 Q9OXG3 PRELIMINARY; PRT; 152 AA.  
 AC Q9OXG3;  
 DT 01-JUN-2003 (TRENBLrel. 24, Created)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)  
 DE Interleukin-2 (Fragment).  
 GN Name=IL2;  
 OS Peromyscus maniculatus (Deer mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;  
 OC Peromyscus.  
 OC NCBI\_TaxID=10042;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Schountz T., Buniger A., Davenport B., Hegg T.;  
 RT "Cloning of deer mouse IL-2, IL-12 p35, IL-21, GM-CSF, CCL3 and CCL4  
 RT cDNAs";  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY247760; AAP04419.1; -;  
 DR HSP; P60568; 1IRL.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005134; F:interleukin-2 receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR009079; 4\_helix\_cytokine.  
 DR InterPro; IPR000779; Interleukin-2.  
 DR Pfam; PF00715; IL2; 1.  
 DR PRINTS; PR00265; INTERLEUKIN2.  
 DR ProDom; PD003649; Interleukin-2; 1.  
 DR SMART; SM00189; IL2; 1.  
 DR PROSITE; PS00424; INTERLEUKIN\_2; 1.  
 FT NON TER 152  
 SQ SEQUENCE 152 AA; 17095 MW; 798D13514AD0CC93 CRC64;

Query Match 72.8%; Score 107; DB 2; Length 152;  
 Best Local Similarity 70.0%; Pred. No. 5.9e-08;  
 Matches 21; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 APTSSSTKKTQLEHLLDQLMILNGINN 30  
 DB 21 APTSSSTKETEQQMEQLLDQLLLGVNN 50

RESULT 28  
 IL2\_RABIT STANDARD; PRT; 153 AA.  
 ID IL2\_RABIT  
 AC O77620;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).  
 GN Name=IL2;  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OC NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=Lymph node;  
 RC MEDLINE=20304414; PubMed=10843729; DOI=10.1006/cyto.1999.0658;  
 RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;  
 RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the  
 RT European rabbit (Oryctolagus cuniculus).";  
 RL Cytokine 12:555-565 (2000).  
 CC -!- FUNCTION: Produced by T-cells in response to antigenic or  
 CC mitogenic stimulation, this protein is required for T-cell  
 CC proliferation and other activities crucial to regulation of the

RA MULLINS-P623904; P.V.M.; Chandrasekar B., Freeman G.L.;  
 RA Melby P.C., Tryon V.V.,  
 RT "Cloning of Syrian hamster (*Mesocricetus auratus*) cytokine cDNAs and  
 RT analysis of cytokine mRNA expression in experimental visceral  
 RT leishmaniasis.";  
 RL Infect. Immun. 66:2135-2142(1998).  
 DR EMBL; AF046212; AAC40097.1; -.  
 DR HSSP; P60568; IRL.  
 DR GO; GO:0005576; C:extracellular; IEA.

CC	1	20	By similarity.
DR	ENBL; M22899; AAA41427.1; -.		
DR	PIR; A45882; A31278.		
DR	HSP; P01585; I449.		
DR	RGD; G20047; IL2.		
DR	InterPro; IPR009079; 4 helix cytokine.		
DR	InterPro; IPR000779; Interleukin-2.		
DR	Pfam; PF00715; IL2; 1.		
DR	PRINTS; PR00265; INTERLEUKIN2.		
DR	ProDom; PD003649; Interleukin-2; 1.		
DR	SMART; SM00189; IL2; 1.		
DR	PROSITE; PS00424; INTERLEUKIN 2; 1.		
KW	Cytokine; Glycoprotein; Growth factor; Immune response; Signal;		
KW	T-cell.		
FT	SIGNAL	1	20 By similarity.

KW  
Cytosol

KW  
 cytokine; glycoprotein; growth factor; immun

KW T-cell.  
 FT SIGNAL 1 20 By similarity.  
 FT CHAIN 21 154 Interleukin-2.  
 FT CARBOHYD 23 23 O-linked (GalNac... ) (By similarity).  
 FT DISULFID 78 126 By similarity.  
 SQ SEQUENCE 154 AA; 17401 MW; F3B95E43DA3D3E1 CRC64;  
  
 Query Match 65.3%; Score 96; DB 1; Length 154;  
 Best Local Similarity 66.7%; Pred. No. 2.8e-06;  
 Matches 20; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
  
 QY 1 APTSSSTKTKTQLEHLHLLDLQMLNGINN 30  
 DB 21 APTSSSTKTKKQLEPLLDLQLLKEVKN 50  
  
 RESULT 34  
 IL2\_MERUN STANDARD; PRT; 155 AA.  
 AC Q8081;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).  
 GN Name=IL2;  
 OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;  
 OC Meriones.  
 OX NCBI\_TaxID=10047;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=94174702; PubMed=8128610; DOI=10.1016/0165-2427(94)90015-9;  
 RA "Mai Z., Kousoulas K.G., Horohov D.W., Klei T.R.;  
 RT "Cross-species PCR cloning of gerbil (Meriones unguiculatus)  
 RT interleukin-2 cDNA and its expression in COS-7 cells.";  
 RL Vet. Immunol. Immunopathol. 40:63-71(1994).  
 CC -!- FUNCTION: Produced by T-cells in response to antigenic or  
 CC mitogenic stimulation, this protein is required for T-cell  
 CC proliferation and other activities crucial to regulation of the  
 CC immune response. Can stimulate B cells, monocytes, lymphokine-  
 CC activated killer cells, natural killer cells, and glioma cells.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the IL-2 family.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; X68779; CAA48679.1; -.  
 DR PIR; S33509; S33509.  
 DR HSP; P01585; 1M49.  
 DR InterPro; IPR009079; 4\_helix\_cytokine.  
 DR InterPro; IPR000779; Interleukin-2.  
 DR Pfam; PF00715; IL2; 1.  
 DR PRINTS; PR00265; INTERLEUKIN2.  
 DR ProDom; PD003649; Interleukin-2; 1.  
 DR SMART; SM00189; IL2; 1.  
 DR PROSITE; PS00424; INTERLEUKIN 2; 1.  
 KW Cytokine; Glycoprotein; Growth factor; Immune response; Signal;  
 T-cell.  
 FT SIGNAL 1 20 By similarity.  
 FT CHAIN 21 155 Interleukin-2.  
 FT CARBOHYD 23 23 O-linked (GalNac... ) (By similarity).  
 FT DISULFID 78 126 By similarity.  
 SQ SEQUENCE 155 AA; 17602 MW; D0F74AAIA381CDDA CRC64;  
  
 Query Match 64.6%; Score 95; DB 1; Length 155;

Best Local Similarity 66.7%; Pred. No. 4e-06;  
 Matches 20; Conservative 2; Mismatches 8; Indels 0; Gaps 0;  
  
 QY 1 APTSSSTKTKTQLEHLHLLDLQMLNGINN 30  
 DB 21 APTSSPAKEAQOYLEQLLDLQLLRGINN 50  
  
 RESULT 35  
 Q865X2 PRELIMINARY; PRT; 154 AA.  
 AC Q865X2;  
 DT 01-JUN-2003 (TREMBLrel. 24, Created)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Interleukin 2.  
 GN Name=IL-2;  
 OS Lama glama (Llama).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.  
 OX NCBI\_TaxID=9844;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Raadan O., Lee S.-., Yoshida R., Chang K.-., Ohashi K., Sugimoto C.,  
 RA Onuma M.;  
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB107651; BAC75388.1; -.  
 DR HSP; P60568; 1IBL.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005134; F:interleukin-2 receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR009079; 4\_helix\_cytokine.  
 DR InterPro; IPR000779; Interleukin-2.  
 DR Pfam; PF00715; IL2; 1.  
 DR PRINTS; PR00265; INTERLEUKIN2.  
 DR ProDom; PD003649; Interleukin-2; 1.  
 DR SMART; SM00189; IL2; 1.  
 DR PROSITE; PS00424; INTERLEUKIN 2; 1.  
 SQ SEQUENCE 154 AA; 17652 MW; 8020EC8DDB7BBA38 CRC64;  
  
 Query Match 63.3%; Score 93; DB 2; Length 154;  
 Best Local Similarity 66.7%; Pred. No. 7.9e-06;  
 Matches 20; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
  
 QY 1 APTSSSTKTKTQLEHLHLLDLQMLNGINN 30  
 DB 21 APTLSSTKTKKQLEPLLDLQLLKEVNN 50  
  
 RESULT 36  
 IL2\_HORSE STANDARD; PRT; 149 AA.  
 ID IL2\_HORSE  
 AC P37997;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).  
 GN Name=IL2;  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94160338; PubMed=8116217; DOI=10.1016/0165-2427(93)90070-K;  
 RA Vandergriff E.V., Horohov D.W.;  
 RT "Molecular cloning and expression of equine interleukin 2.";  
 RL Vet. Immunol. Immunopathol. 39:395-406(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Tavernor A.S., Allen W.R., Butcher G.W.;  
 RL Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Produced by T-cells in response to antigenic or

```
CC mitogenic stimulation, this protein is required for T-cell
CC proliferation and other activities crucial to regulation of the
CC immune response. Can stimulate B cells, monocytes, lymphokine-
CC activated killer cells, natural killer cells, and glioma cells.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-2 family.
CC -----
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CC -----
DR EMBL; L06009; AAA20134.1; -
DR EMBL; X69393; CAA49190.1; -
DR PIR; S31391; S31391.
DR HSSP; P01585; 1M47.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
DR Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
KW T-cell.
FT SIGNAL 1 20 By similarity.
FT CHAIN 21 149 Interleukin-2.
FT DISULFID 78 121 By similarity.
FT CARBOHYD 23 23 O-linked (GalNAc. . .) (By similarity).
FT CARBOHYD 106 106 N-linked (GlcNAc. . .) (Potential).
FT CONFLICT 3 3 R -> K (in Ref. 2).
FT CONFLICT 8 8 S -> A (in Ref. 2).
FT CONFLICT 59 59 I -> M (in Ref. 2).
FT CONFLICT 125 125 N -> D (in Ref. 2).
FT CONFLICT 128 128 E -> G (in Ref. 2).
FT CONFLICT 145 145 I -> F (in Ref. 2).
FT CONFLICT 148 148 L -> M (in Ref. 2).
SQ SEQUENCE 149 AA; 17086 MW; 051BB8C47A0114FC CRC64;

Query Match 62.6%; Score 92; DB 1; Length 149;
Best Local Similarity 56.7%; Pred. No. 1,1e-05;
Matches 17; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 APTSSSTKTKTQLQLEHLLDLQMLNGINN 30
Db 21 APTSSSKRETQQLKQLQMLDLKLLGVNN 50

RESULT 37
Q9UCF5 PRELIMINARY; PRT; 23 AA.
AC Q9UCF5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Interleukin 2 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93289963; PubMed=8512072; DOI=10.1006/abio.1993.1209;
RA Mullner S., Karbe-Thonges B., Tripler D.;
RT "Charge heterogeneity of insulin fusion proteins expressed in
RT Escherichia coli is not due to proteolytic degradation.";
RL Anal. Biochem. 210:366-373(1993).
SQ SEQUENCE 23 AA; 2637 MW; 40B64C6875CE021F CRC64;

Query Match 61.9%; Score 91; DB 2; Length 23;
```

```
Best Local Similarity 90.5%; Pred. No. 1.9e-06;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TSSSTKTKTQLQLEHLLDLQML 23
Db 3 TSXSTKTKTQLQLEHLLDLQML 23

RESULT 38
IL2_ORCOR
ID IL2_ORCOR STANDARD; PRT; 152 AA.
AC Q97513;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGFP
DE (Fragment)).
DE Name=IL2;
OS Orcinus orca (Killer whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Orcinus.
OX NCBI_TaxID=9733;
RN [1]
RP SEQUENCE FROM N.A.
RA Ness T.L., Bradley W.G., Reynolds J.E. III, Roess W.B.;
RT "Isolation and expression of the interleukin-2 gene from the killer
RT whale, Orcinus orca.";
RL Mar. Mamm. Sci. 14:531-543(1998).
CC -!- FUNCTION: Produced by T-cells in response to antigenic or
CC mitogenic stimulation, this protein is required for T-cell
CC proliferation and other activities crucial to regulation of the
CC immune response. Can stimulate B cells, monocytes, lymphokine-
CC activated killer cells, natural killer cells, and glioma cells (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-2 family.
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CC -----
DR EMBL; AF009570; AAD01426.1; -
DR HSSP; P01585; 1M49.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
DR Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
KW T-cell.
FT SIGNAL 1 20 By similarity.
FT CHAIN 21 >152 Interleukin-2.
FT CARBOHYD 23 23 O-linked (GalNAc. . .) (By similarity).
FT DISULFID 78 126 By similarity.
FT NON_TER 152 152
SQ SEQUENCE 152 AA; 17424 MW; 308F91821ECCB764 CRC64;

Query Match 59.9%; Score 88; DB 1; Length 152;
Best Local Similarity 60.0%; Pred. No. 4.5e-05;
Matches 18; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 APTSSSTKTKTQLQLEHLLDLQMLNGINN 30
Db 21 APTSSSTNTKKQVQSLLQDLKLLKEINN 50
```



## RESULT 39

Q71V48  
ID Q71V48 PRELIMINARY; PRT; 38 AA.  
AC Q71V48;  
DT 05-JUL-2004 (TREMELrel. 27, Created)  
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)  
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)  
DE Interleukin-2 (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Turner D.M., Sinnott P.J., Hutchinson I.V.;  
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF031845; BAB86861.1; -  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005134; F:interleukin-2 receptor binding; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR000779; Interleukin-2.  
DR Pfam; PF00715; IL2; 1.  
DR ProDom; PD003649; Interleukin-2; 1.  
FT NON\_TER 38 38  
SQ SEQUENCE 38 AA; 4192 MW; 8DE4AE5344C2CBA3 CRC64;

Query Match 59.2%; Score 87; DB 2; Length 38;  
Best Local Similarity 100.0%; Pred. No. 1.3e-05; Mismatches 0; Indels 0; Gaps 0;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLL 18  
DB 21 APTSSSTKKTQLEHLL 38  
|||||

## RESULT 40

Q9XT84  
ID Q9XT84 PRELIMINARY; PRT; 154 AA.  
AC Q9XT84;  
DT 01-NOV-1999 (TREMELrel. 12, Created)  
DT 01-NOV-1999 (TREMELrel. 12, Last sequence update)  
DT 01-WAR-2004 (TREMELrel. 26, Last annotation update)  
DE Interleukin 2.  
OS Delphinapterus leucas (Beluga whale).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;  
OC Monodontidae; Delphinapterus.  
OX NCBI\_TaxID=9749;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99221046; PubMed=10206205; DOI=10.1016/S0165-2427(99)00009-4;  
RA St-Laurent G., Beliveau C., Archambault D.;  
RT "Molecular cloning and phylogenetic analysis of beluga whale  
RT (Delphinapterus leucas) and grey seal (Halichoerus grypus) interleukin  
RT 2.";  
RL Vet. Immunol. Immunopathol. 67:385-394(1999).  
DR EMBL; AF072870; AAD40847.1; -  
DR HSP; P60568; IRL.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005134; F:interleukin-2 receptor binding; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR009079; 4 helix cytokine.  
DR InterPro; IPR000779; Interleukin-2.  
DR Pfam; PF00715; IL2; 1.  
DR PRINTS; PR00285; INTERLEUKIN2.  
DR ProDom; PD003649; Interleukin-2; 1.  
DR SMART; SM00189; IL2; 1.  
DR PROSITE; PS00424; INTERLEUKIN\_2; 1.  
SQ SEQUENCE 154 AA; 17652 MW; 4288D3D41D04F172 CRC64;

Query Match 56.5%; Score 83; DB 2; Length 154;  
Best Local Similarity 56.7%; Pred. No. 0.0026;  
Matches 17; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQLEHLLDLQMLNGINN 30  
DB 21 APTSSSTKKTQVQSLLQDLHLKKEINN 50  
|||||

Search completed: September 23, 2005, 12:48:04  
Job time : 52.1475 secs

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OM protein - protein search, using sw model

Run on: September 23, 2005, 12:40:19 ; Search time 23.6066 Seconds  
(without alignments)  
122.275 Million cell updates/sec

Title: US-10-727-514-4

Perfect score: 147

Sequence: 1 APTSSSTKTKQLQLEHLLDLQMLNGINN 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	147	100.0	153	1	ICG12
2	147	100.0	153	1	ICHU2
3	114	77.6	154	2	JN0698
4	97	66.0	155	2	A31278
5	96	65.3	154	2	S16241
6	95	64.6	155	2	S33509
7	92	62.6	149	2	S31391
8	79	53.7	155	2	I45913
9	79	53.7	155	2	S38662
10	79	53.7	155	2	S11488
11	69	46.9	169	1	S37289
12	64	43.5	169	1	ICMS2
13	59.5	40.5	60	2	I68870
14	58.5	39.8	62	2	I54512
15	57.5	39.1	72	2	I68871
16	54	36.7	357	2	S12169
17	52	35.4	737	2	G82262
18	51	34.7	304	2	F95285
19	51	34.7	627	2	E70122
20	50	34.0	365	2	C70701
21	49	33.3	543	2	F82217
22	49	33.3	1130	2	A89130
23	48.5	33.0	240	2	T22210
24	48	32.7	155	1	F64145
25	48	32.7	189	2	H64307
26	48	32.7	441	2	AB1367
27	48	32.7	441	2	AC1736
28	48	32.7	1061	1	GNLJG4
29	47.5	32.3	244	2	T11685

30	47.5	32.3	938	2	F86548
31	47.5	32.3	938	2	H72074
32	47	32.0	230	2	H82447
33	47	32.0	398	2	B70209
34	47	32.0	557	2	F89839
35	47	32.0	1008	2	T41244
36	47	32.0	1964	2	A59282
37	46.5	31.6	159	2	T05656
38	46.5	31.6	211	2	C84888
39	46	31.3	293	2	A71946
40	46	31.3	323	2	H90434
41	46	31.3	380	1	C37760
42	46	31.3	516	2	B64551
43	46	31.3	571	2	H82355
44	46	31.3	614	2	T18745
45	46	31.3	692	2	T32980
46	46	31.3	1612	2	JC5210
47	46	31.3	3724	2	T18427
48	45.5	31.0	466	2	E90228
49	45	30.6	307	2	T46103
50	45	30.6	328	2	AC2415
51	45	30.6	333	2	S32114
52	45	30.6	343	2	C89779
53	45	30.6	530	2	C82442
54	45	30.6	870	1	GNMVJA
55	45	30.6	895	2	F75608
56	45	30.6	903	2	JR0327
57	45	30.6	903	2	T50334
58	45	30.6	1802	2	G71616
59	44.5	30.3	359	2	T22950
60	44.5	30.3	511	2	S44275
61	44.5	30.3	741	2	A45771
62	44	29.9	269	2	G91169
63	44	29.9	273	2	G86015
64	44	29.9	283	2	B97167
65	44	29.9	324	2	A97036
66	44	29.9	347	2	A12010
67	44	29.9	357	2	S23526
68	44	29.9	357	2	S23525
69	44	29.9	368	2	T46607
70	44	29.9	474	2	B69494
71	44	29.9	474	2	A11146
72	44	29.9	581	2	S09140
73	44	29.9	585	2	T19814
74	44	29.9	594	2	A86309
75	44	29.9	595	2	JC8012
76	44	29.9	627	2	S46820
77	44	29.9	628	2	B91146
78	44	29.9	628	2	F85991
79	44	29.9	715	2	G86634
80	44	29.9	752	2	D40899
81	44	29.9	943	2	S44636
82	44	29.9	1019	2	T11560
83	44	29.9	1034	2	D65119
84	44	29.9	1050	2	AE0380
85	44	29.9	1182	2	T30189
86	44	29.9	1187	2	T46637
87	44	29.9	1188	2	T46608
88	44	29.9	1245	2	E83110
89	43.5	29.6	115	2	D97846
90	43.5	29.6	289	1	S56226
91	43.5	29.6	337	1	A37760
92	43	29.3	145	2	H83921
93	43	29.3	152	2	T04479
94	43	29.3	184	2	D71933
95	43	29.3	202	2	S75332
96	43	29.3	209	2	H69901
97	43	29.3	210	2	B85594
98	43	29.3	210	2	F64821
99	43	29.3	210	2	F90743
100	43	29.3	253	2	T15385

polymorphic outer  
polymorphic membra  
DNA-binding respon  
conserved hypotet  
hypothetical prote  
SEC14 protein homo  
nonmuscle myosin I  
hypothetical prote  
hypothetical prote  
hypothetical prote  
galactokinase (EC  
oligopeptide ABC t  
peptide ABC transp  
hypothetical prote  
hypothetical prote  
DNA (cytosine-5)-  
hypothetical prote  
amino acid specifi  
hypothetical prote  
85C protein - Myco  
hypothetical prote  
probable peptide A  
pol polyprotein -  
conserved hypotet  
dynam-in-related pr  
dynam-in-related pr  
hypothetical prote  
hypothetical prote  
dopamine receptor  
2-5A-dependent RNA  
probable acyltrans  
hypothetical prote  
flagellin family P  
probable membrane  
two-component hybr  
cinnamyl-alcohol d  
cinnamyl-alcohol d  
3-isopropylmalate  
phenylalanyl-trNA  
hypothetical cell  
coli intron prote  
hypothetical prote  
F20D23.3 protein -  
G protein-coupled  
hypothetical prote  
probable integral  
probable integral  
hypothetical prote  
pol polyprotein -  
f22b7.5 protein -  
pol polyprotein -  
acriflavin resista  
multidrug efflux p  
myelin transcripti  
transcription fact  
zinc finger protei  
exodeoxyribonuclea  
hypothetical prote  
hypothetical prote  
UDPglucose 4-epime  
transcription regu  
cinnamyl-alcohol d  
hypothetical prote  
fibrillin - Synech  
general stress pro  
probable transfera  
probable glutathio  
probable transfera  
hypothetical prote

## ALIGNMENTS

## RESULT 1

ICG12

interleukin-2 precursor - common gibbon  
 N:Alternate names: IL-2; T-cell growth factor  
 C:Species: Hylobates lar (common gibbon, white-handed gibbon)  
 C>Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004  
 C:Accession: A94067; A01849  
 R:Chen, S.J.; Holbrook, N.J.; Mitchell, K.F.; Vallone, C.A.; Greengard, J.S.; Crabtree, Proc. Natl. Acad. Sci. U.S.A. 82, 7284-7288, 1985  
 A:Title: A viral long terminal repeat in the interleukin 2 gene of a cell line that contains a provirus  
 A:Reference number: A94067; MUID:86042650; PMID:3877307  
 A:Accession: A94067  
 A:Molecule type: mRNA  
 A:Residues: 1-153 <CHE>  
 A:Cross-references: UNIPROT:P60569; GB:M11144; NID:G177014; PIDN:AAA35454.1; PID:G177015  
 A:Experimental source: leukemia cell line M1A 144; ATCC TIB 201  
 C>Note: the integration of a retrovirus sequence containing a 5' LTR into the 3' noncoding region of the interleukin-2 gene  
 C:Superfamily: interleukin-2  
 C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-153/Product: interleukin-2 #status predicted <IL2>  
 F:23/Binding site: carboxylate (Thr) (covalent) #status predicted  
 F:78-125/Disulfide bonds: #status predicted

Query Match 100.0%; Score 147; DB 1; Length 153;  
 Best Local Similarity 100.0%; Pred. NO. 2.3e-14;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSSSTKTKQLQLEHLLDLQMLNGINN 30  
 DB 21 APTSSSTKTKQLQLEHLLDLQMLNGINN 50

## RESULT 2

ICHU2

interleukin-2 precursor [validated] - human  
 N:Alternate names: IL-2; T-cell growth factor  
 C:Species: Homo sapiens (man)  
 C>Date: 11-Aug-1983 #sequence\_revision 11-Aug-1983 #text\_change 09-Jul-2004  
 R:Holbrook, N.J.; Lieber, M.; Crabtree, G.R. Proc. Natl. Acad. Sci. U.S.A. 80, 7437-7441, 1983  
 A:Title: Structure of the human interleukin 2 gene.  
 A:Reference number: A21192; MUID:84170243; PMID:6324170  
 A:Accession: A21192  
 A:Molecule type: DNA  
 A:Residues: 1-153 <HOL>  
 A:Cross-references: UNIPROT:P60568; GB:X00695; GB:X00200; GB:X00201; GB:X00202; NID:G33781  
 R:Fujita, T.; Takaoka, C.; Matsui, H.; Taniguchi, T. Proc. Natl. Acad. Sci. U.S.A. 80, 7437-7441, 1983  
 A:Title: Structure of the human interleukin 2 gene.  
 A:Reference number: A21192; MUID:84170243; PMID:6324170  
 A:Accession: A21192  
 A:Molecule type: DNA  
 A:Residues: 1-153 <FUG>  
 A:Cross-references: GB:J00264; NID:G186294; PIDN:AAD48509.1; PID:G5729676  
 R:Holbrook, N.J.; Smith, K.A.; Fornace Jr., A.J.; Comeau, C.M.; Wiskocil, R.L.; Crabtree, Proc. Natl. Acad. Sci. U.S.A. 81, 1634-1638, 1984  
 A:Title: T-cell growth factor: complete nucleotide sequence and organization of the gene  
 A:Reference number: A20961; MUID:84170356; PMID:6608729  
 A:Accession: A20961  
 A:Molecule type: DNA  
 A:Residues: 1-153 <HO2>  
 A:Cross-references: GB:K02056; NID:G186302; PIDN:AAA98792.1; PID:G386819  
 R:Laabi, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, EMBO J. 11, 3897-3904, 1992  
 A:Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;12)(p11;p11) translocation  
 A:Reference number: S31208; MUID:93010984; PMID:1396583  
 A:Accession: S31209  
 A:Molecule type: mRNA  
 A:Note: mutation of Phe-42 to Ala reduced binding to the IL-2 receptor 5-10 fold without

A:Residues: 11-117 <LAA>  
 A:Cross-references: EMBL:Z14955  
 A:Note: this sequence is shown from the beginning of the fragment to the chromosomal break  
 R:Taniguchi, T.; Matsui, H.; Fujita, T.; Takaoka, C.; Kashima, N.; Yoshimoto, R.; Hamuro Nature 302, 305-310, 1983  
 A:Title: Structure and expression of a cloned cDNA for human interleukin-2.  
 A:Reference number: A93297; MUID:83167472; PMID:6403867  
 A:Accession: A93297  
 A:Molecule type: mRNA  
 A:Residues: 1-153 <TAN>  
 A:Cross-references: GB:V00564; NID:G33780; PIDN:CAA23827.1; PID:G33781  
 A:Experimental source: leukemic T-cell line Jurkat-111, cloned from Jurkat-FHCRC  
 R:Mada, S.; Nishino, N.; Obaru, K.; Mita, S.; Nomiya, H.; Shimada, K.; Fujimoto, K.; Biochem. Biophys. Res. Commun. 115, 1040-1047, 1983  
 A:Title: Cloning of interleukin 2 mRNAs from human tonsils.  
 A:Reference number: A90113; MUID:84023840; PMID:6312994  
 A:Accession: A90113  
 A:Molecule type: mRNA  
 A:Residues: 1-153 <MAB>  
 A:Cross-references: GB:J00264; NID:G186294; PIDN:AAD48509.1; PID:G5729676  
 A:Experimental source: tonsillar mononuclear cells  
 R:Devos, R.; Plaetinck, G.; Cheroutre, H.; Simons, G.; Degraeve, W.; Tavernier, J.; Renau Nucleic Acids Res. 11, 4307-4323, 1983  
 A:Title: Molecular cloning of human interleukin 2 cDNA and its expression in Escherichia coli  
 A:Reference number: A93478; MUID:83246551; PMID:6306584  
 A:Accession: A93478  
 A:Molecule type: mRNA  
 A:Residues: 1-153 <DEV>  
 A:Cross-references: GB:V00564; NID:G33780; PIDN:CAA23827.1; PID:G33781  
 A:Experimental source: splenocytes  
 R:Eisenberg, O.; Faber-Elman, A.; Lotan, M.; Schwartz, M. J. Neurochem. 64, 1928-1936, 1995  
 A:Title: Interleukin-2 transcripts in human and rodent brains: possible expression by as  
 A:Reference number: I56518; MUID:95239150; PMID:7722480  
 A:Accession: I56518  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-152 <EIZ>  
 A:Cross-references: GB:S77834; NID:G999000  
 A:Accession: I73624  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 5-7, 'P', 9-17, 'P', 19-32, 'X', 34-45, 'X', 47-143 <RES>  
 A:Cross-references: GB:S77835; NID:G999001; PIDN:AAD14264.1; PID:G4261964  
 R:Nishino, N.; Obaru, K.; Maeda, S.; Shimada, K.; Onoue, K. Biomed. Res. 6, 197-205, 1985  
 A:Title: Organization of the DNA regions flanking the human interleukin 2 gene.  
 A:Reference number: I52528  
 A:Accession: I52528  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-68 <RE2>  
 A:Cross-references: GB:M33199; NID:G186296; PIDN:AAA59139.1; PID:G553508  
 R:Siebelist, U.; Durand, D.B.; Bressler, P.; Holbrook, N.J.; Norris, C.A.; Kamoun, M.; Mol. Cell. Biol. 6, 3042-3049, 1986  
 A:Title: Promoter region of interleukin-2 gene undergoes chromatin structure changes and  
 A:Reference number: I57603; MUID:87064618; PMID:3491296  
 A:Accession: I57603  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-68 <RE3>  
 A:Cross-references: GB:M13879; NID:G186305; PIDN:AAA59141.1; PID:G553509  
 R:Weir, M.P.; Chaplin, M.A.; Wallace, D.M.; Dykes, C.W.; Hobden, A.N. Biochemistry 27, 6883-6892, 1988  
 A:Title: Structure-activity relationships of recombinant human interleukin 2.  
 A:Reference number: I52401; MUID:89062420; PMID:3264184  
 A:Contents: recombinant IL-2 and mutants expressed in E. coli  
 A:Accession: I52401  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 'M', 21-153 <REA>  
 A:Cross-references: GB:M22005; NID:G186300; PIDN:AAA59140.1; PID:G386818  
 A:Note: mutation of Phe-42 to Ala reduced binding to the IL-2 receptor 5-10 fold without

R;Robb, R.J.; Kutny, R.M.; Panico, M.; Morris, H.R.; Chowdhry, V.  
Proc. Natl. Acad. Sci. U.S.A. 81, 6486-6490, 1984  
A;Title: Amino acid sequence and post-translational modification of human interleukin 2.  
A;Reference number: A94009; MUID:85038540; PMID:6333684  
A;Accession: A94009  
A;Molecule type: protein  
A;Residues: 21-153 <ROB>  
A;Note: disulfide bonds and carbohydrate binding site were determined  
n in lacking 21-Ala (FT-IL2-A and FT-IL2-B) and 22-Pro (FT-IL2-B)  
R;Conradt, H.S.; Nimtz, M.; Dittmar, K.E.J.; Lindenmaier, W.; Hoppe, J.; Hauser, H.  
J. Biol. Chem. 264, 17368-17373, 1989  
A;Title: Expression of human interleukin-2 in recombinant baby hamster kidney, Ltk-, and  
de.  
A;Reference number: A34463; MUID:90008901; PMID:2793860  
A;Accession: A34463  
A;Molecule type: protein  
A;Residues: 21-35 <CON>  
A;Note: the O-linked glycosylation site in recombinant material matched that from human  
R;Grabenhorst, E.; Hofer, B.; Nimtz, M.; Jaeger, V.; Conradt, H.S.  
Eur. J. Biochem. 215, 189-197, 1993  
A;Title: Biosynthesis and secretion of human interleukin 2 glycoproteins variants from B  
A;Reference number: S34052; MUID:93345493; PMID:8344280  
A;Contents: annotation; Glycosylation of variant forms expressed in insect cells  
C;Genetics:  
A;Gene: GDB:IL2  
A;Cross-references: GDB:119344; OMIM:147680  
A;Map position: 4q26-q27  
A;Introns: 49/3; 63/3; 117/3  
C;Superfamily: interleukin-2  
C;Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-153/Product: interleukin-2 #status experimental <IL2>  
F;23/Binding site: carbohydrate (Thr) (covalent) #status experimental  
F;78-125/Disulfide bonds: #status experimental

Query Match 100.0%; Score 147; DB 1; Length 153;  
Best Local Similarity 100.0%; Pred. No. 2.3e-14;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQQLLEHLLDLQMLINGNN 30  
DB 21 APTSSSTKKTQQLLEHLLDLQMLINGNN 50

RESULT 3  
JN0698  
interleukin 2 precursor - cat  
C;Species: Felis silvestris catus (domestic cat)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004  
C;Accession: JN0698  
R;Cozzi, P.J.; Padrid, P.A.; Takeda, J.; Alegria, M.L.; Yuhki, N.; Leff, A.R.  
Biochem. Biophys. Res. Commun. 194, 1038-1043, 1993  
A;Title: Sequence and functional characterization of feline interleukin 2.  
A;Reference number: JN0698; MUID:93356765; PMID:8352761  
A;Accession: JN0698  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-154 <COZ>  
A;Cross-references: UNIPROT:Q07885; GB:L19402; NID:G304313; PIDN:AAA02865.1; PID:G304314  
C;Superfamily: interleukin-2  
C;Keywords: growth factor

Query Match 77.6%; Score 114; DB 2; Length 154;  
Best Local Similarity 73.3%; Pred. No. 1.8e-09;  
Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQQLLEHLLDLQMLINGNN 30  
DB 21 APASSTKETQQLLEHLLDLQMLINGNN 50

RESULT 4

A31278  
interleukin-2 precursor - rat  
N;Alternate names: IL-2; T-cell growth factor  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 26-Apr-1989 #sequence\_revision 26-Apr-1989 #text\_change 09-Jul-2004  
C;Accession: A45882; A31278  
R;McKnight, A.J.; Mason, D.W.; Barclay, A.N.  
Immunogenetics 30, 145-147, 1989  
A;Title: Sequence of rat interleukin 2 and anomalous binding of a mouse interleukin 2 c  
A;Reference number: A45882; MUID:89339608; PMID:2788130  
A;Accession: A45882  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-155 <MC>  
A;Cross-references: UNIPROT:P17108; GB:M22899; NID:G204909; PIDN:AAA41427.1; PID:G204910  
C;Superfamily: interleukin-2  
C;Keywords: cytokine; glycoprotein; growth factor; immunoregulation; T-cell

Query Match 66.0%; Score 97; DB 2; Length 155;  
Best Local Similarity 66.7%; Pred. No. 6e-07;  
Matches 20; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQQLLEHLLDLQMLINGNN 30  
DB 21 APTSSPAKETQQLLEHLLDLQMLINGNN 50

RESULT 5  
S16241  
interleukin-2 precursor - pig  
N;Alternate names: IL-2; T-cell growth factor  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C;Accession: S16241; S15473  
R;Goodall, J.C.; Emery, D.C.; Bailey, M.; English, L.S.; Hall, L.  
Biochim. Biophys. Acta 1089, 257-258, 1991  
A;Title: cDNA cloning of porcine interleukin 2 by polymerase chain reaction.  
A;Reference number: S16241; MUID:91274360; PMID:2054386  
A;Accession: S16241  
A;Molecule type: mRNA  
A;Residues: 1-154 <GOO>  
A;Cross-references: UNIPROT:P26891; EMBL:X56750; NID:G1991; PIDN:CAA40071.1; PID:G1992  
R;Lefevre, F.  
A;Description: Molecular cloning of porcine interleukin 2 cDNA by the polymerase chain  
submitted to the EMBL Data Library, March 1991  
A;Reference number: S15473  
A;Accession: S15473  
A;Molecule type: mRNA  
A;Residues: 1-154 <LEP>  
A;Cross-references: EMBL:X58428; NID:G2068; PIDN:CAA41330.1; PID:G2069  
C;Superfamily: interleukin-2  
C;Keywords: cytokine; glycoprotein; growth factor; immunoregulation; T-cell  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-154/Product: interleukin-2 #status predicted <MAT>

Query Match 65.3%; Score 96; DB 2; Length 154;  
Best Local Similarity 66.7%; Pred. No. 8.4e-07;  
Matches 20; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQQLLEHLLDLQMLINGNN 30  
DB 21 APTSSSTKKTQQLLEHLLDLQMLINGNN 50

RESULT 6  
S33509  
interleukin-2 - Mongolian jird  
C;Species: Meriones unguiculatus (Mongolian jird)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S33509  
R;Mai, Z.; Klei, T.; Horchov, D.  
submitted to the EMBL Data Library, October 1992  
A;Description: Cross-species PCR cloning of Jird (Meriones unguiculatus) interleukin-2 c

A;Reference number: S33509  
 A;Accession: S33509  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-155 <MAI>  
 A;Cross-references: UNIPROT:Q08081; EMBL:X68779; NID:g577588; PIDN:CAA48679.1; PID:g3116  
 C;Superfamily: interleukin-2

Query Match 64.6%; Score 95; DB 2; Length 155;  
 Best Local Similarity 66.7%; Pred. No. 1.2e-06;  
 Matches 20; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQQLQLEHLLDLQMLINGINN 30  
 ||||| |::| |||||::| |:  
 Db 21 APTSPFAKEAQQYLEQLLLDLQLLRGINN 50

## RESULT 7

S31391  
 interleukin-2 precursor - horse  
 C;Species: Equus caballus (domestic horse)  
 C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
 C;Accession: S31391  
 R;Tavernor, A.S.; Butcher, G.W.  
 submitted to the EMBL Data Library, November 1992  
 A;Description: cDNA cloning of equine interleukin-2 by polymerase chain reaction.  
 A;Reference number: S31391  
 A;Accession: S31391  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-149 <TAV>  
 A;Cross-references: UNIPROT:P37997; EMBL:X69393; NID:g1076; PIDN:CAA49190.1; PID:g1077  
 C;Superfamily: interleukin-2

Query Match 62.6%; Score 92; DB 2; Length 149;  
 Best Local Similarity 56.7%; Pred. No. 3.2e-06;  
 Matches 17; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQQLQLEHLLDLQMLINGINN 30  
 ||||| |::| ||::|::| |:  
 Db 21 APTSSSKRETQQLQQLQMDLKLLEGVNN 50

## RESULT 8

I45913  
 interleukin-2 precursor - bovine  
 C;Species: Bos primigenius taurus (cattle)  
 C;Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004  
 C;Accession: I45913; S21470; S20761  
 R;Cerretti, D.P.; McKereghan, K.; Larsen, A.; Cantrell, M.A.; Anderson, D.; Gillis, S.; Proc. Natl. Acad. Sci. U.S.A. 83, 3223-3227, 1986  
 A;Title: Cloning, sequence, and expression of bovine interleukin 2.  
 A;Reference number: I45913; MUID:86205869; PMID:3517854  
 A;Accession: I45913  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-155 <CER>  
 A;Cross-references: UNIPROT:P05016; GB:M12791; NID:g163204; PIDN:AAA30586.1; PID:g163205  
 R;Anikeeva, N.N.; Vinogradova, T.V.; Votozhin, O.N.  
 submitted to the EMBL Data Library, December 1989  
 A;Reference number: S21470  
 A;Accession: S21470  
 A;Molecule type: DNA  
 A;Residues: 1-22 <AN2>  
 A;Cross-references: EMBL:X17201; NID:g452; PIDN:CAA35062.1; PID:g453  
 C;Genetics:  
 A;Gene: IL-2  
 C;Superfamily: interleukin-2  
 C;Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell

Query Match 53.7%; Score 79; DB 2; Length 155;  
 Best Local Similarity 53.3%; Pred. No. 0.00028;  
 Matches 16; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQQLQLEHLLDLQMLINGINN 30  
 ||||| |::| |||||::| |:  
 Db 21 APTSSSTGNTMKVKSLLLDLQLLEKVKN 50

## RESULT 9

S38662  
 interleukin-2 - goat  
 C;Species: Capra aegagrus hircus (domestic goat)  
 C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
 C;Accession: S38662  
 R;Rimstad, E.  
 submitted to the EMBL Data Library, November 1993  
 A;Description: The molecular cloning and expression of caprine interleukin 2.  
 A;Reference number: S38662  
 A;Accession: S38662  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-155 <RIM>  
 A;Cross-references: UNIPROT:P36835; EMBL:X76063; NID:g416002; PIDN:CAA53664.1; PID:g4160  
 C;Superfamily: interleukin-2

Query Match 53.7%; Score 79; DB 2; Length 155;  
 Best Local Similarity 53.3%; Pred. No. 0.00028;  
 Matches 16; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQQLQLEHLLDLQMLINGINN 30  
 ||||| |::| |||||::| |:  
 Db 21 APTSSSTGNTMKVKSLLLDLQLLEKVKN 50

## RESULT 10

S11488  
 interleukin-2 precursor - sheep  
 C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C;Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
 C;Accession: S11488; S13102; S15517  
 R;Goodall, J.C.; Emery, D.C.; Ferry, A.C.F.; English, L.S.; Hall, L. Nucleic Acids Res. 18, 5883, 1990  
 A;Title: cDNA cloning of ovine interleukin 2 by PCR.  
 A;Reference number: S11488; MUID:91016933; PMID:2216781  
 A;Accession: S11488  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-155 <GOO>  
 A;Cross-references: UNIPROT:P19114; EMBL:X53934; NID:g1281; PIDN:CAA37881.1; PID:g1282  
 R;Seow, H.F.; Rothel, J.S.; Radford, A.J.; Wood, P.R. Nucleic Acids Res. 18, 7175, 1990  
 A;Title: The molecular cloning of ovine interleukin 2 gene by the polymerase chain react  
 A;Reference number: S13102; MUID:91088336; PMID:2263496  
 A;Accession: S13102  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-5, 'L', 7-155 <SEO>  
 A;Cross-references: EMBL:X55641; NID:g1810; PIDN:CAA39165.1; PID:g1811  
 R;Bujdosó, R.; Williamson, M.L.; Sargan, D.R.; Hein, W.H.; McConnell, I. submitted to the EMBL Data Library, April 1991  
 A;Reference number: S15517  
 A;Accession: S15517  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 21-153 <BOJ>  
 A;Cross-references: EMBL:X60148  
 C;Superfamily: interleukin-2

Query Match 53.7%; Score 79; DB 2; Length 155;  
 Best Local Similarity 53.3%; Pred. No. 0.00028;  
 Matches 16; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQQLQLEHLLDLQMLINGINN 30  
 ||||| |::| |||||::| |:  
 Db 21 APTSSSTGNTMKVKSLLLDLQLLEKVKN 50







A;Contents: annotation  
C;Genetics:  
A;Gene: Sma0353  
A;Genome: plasmid

Query Match 34.7%; Score 51; DB 2; Length 304;  
Best Local Similarity 48.1%; Pred. No. 8.4;  
Matches 13; Conservative 5; Mismatches 7; Indels 2; Gaps 1;

QY 6 STKKTQQLQLE-HLLLDLQMLNGINN 30  
||||| : : : : :  
Db 58 STKKPQLTQLEGRVLAARSVSGIND 84

## RESULT 19

E70122  
flagellar hook-associated protein (flgK) homolog - Lyme disease spirochete  
C;Species: Borrelia burgdorferi (lyme disease spirochete)  
C;Date: 13-Feb-1998 #sequence\_revision 13-Feb-1998 #text\_change 09-Jul-2004  
C;Accession: E70122  
R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White  
son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,  
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.  
Nature 390, 580-586, 1997  
A;Authors: Smith, H.O.; Venter, J.C.  
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.  
A;Reference number: A70100; MUID:98065943; PMID:9403685  
A;Accession: E70122  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-627 <KLE>  
A;Cross-references: UNIPROT:P70859; GB:AE001129; GB:AE000783; NID:g2688071; PIDN:AAC6657  
A;Experimental source: strain B31

Query Match 34.7%; Score 51; DB 2; Length 627;  
Best Local Similarity 42.3%; Pred. No. 19;  
Matches 11; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 4 SSSTKKTQQLQLEHLLLDLQMLNGIN 29  
| : : : : :  
Db 564 SEITKESQSKLDLTLDRMSISGVN 589

## RESULT 20

C70701  
hypothetical protein Rv0029 - Mycobacterium tuberculosis (strain H37RV)  
C;Species: Mycobacterium tuberculosis  
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 09-Jul-2004  
C;Accession: C70701  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.  
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A;Reference number: A70500; MUID:98295987; PMID:9634230  
A;Accession: C70701  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-365 <COL>  
A;Cross-references: UNIPROT:P71599; GB:Z80233; GB:AL123456; NID:g3261645; PIDN:CAB02414.  
A;Experimental source: strain H37RV  
C;Genetics:  
A;Gene: Rv0029

Query Match 34.0%; Score 50; DB 2; Length 365;  
Best Local Similarity 40.0%; Pred. No. 15;  
Matches 12; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 1 APTSSSTKKTQQLQLEHLLLDLQMLNGINN 30  
| : : : : :  
Db 43 AELSSNTAETATLAELKADLRHVGSAND 72

## RESULT 21

F82217  
methyl-accepting chemotaxis protein VC1298 [imported] - Vibrio cholerae (strain N16961)  
C;Species: Vibrio cholerae  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
C;Accession: F82217  
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I.;  
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A;Reference number: A82035; MUID:20406833; PMID:10952301  
A;Accession: F82217  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-543 <HEI>  
A;Cross-references: UNIPROT:Q9KSF8; GB:AE004209; GB:AE003852; NID:g9655779; PIDN:AAF944.  
A;Experimental source: serogroup O1, strain N16961; biotype El Tor  
C;Genetics:  
A;Gene: VC1298  
A;Map position: 1

Query Match 33.3%; Score 49; DB 2; Length 543;  
Best Local Similarity 37.5%; Pred. No. 32;  
Matches 9; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 3 TSSSTKKTQQLQLEHLLLDLQMLN 26  
| : : : : :  
Db 506 SASETREISIDLEHLSQQLLESLN 529

## RESULT 22

A89130  
protein F52E1.4 [imported] - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 24-May-2001  
C;Accession: A89130  
R;anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolo  
A;Reference number: A75000; MUID:99069613; PMID:9851916  
A;Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_el  
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; an  
A;Accession: A89130  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1130 <STO>  
A;Cross-references: GB:chr\_V; PIDN:AAB37038.1; PID:g1086805; GSPDB:GN00023; CESP:F52E1.4  
C;Genetics:  
A;Gene: F52E1.4  
A;Map position: 5  
C;Superfamily: membrane-bound guanylate cyclase; guanylate cyclase catalytic domain hom

Query Match 33.3%; Score 49; DB 2; Length 1130;  
Best Local Similarity 46.2%; Pred. No. 72;  
Matches 12; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 3 TSSSTKKTQQLQLEHLLLDLQMLNGI 28  
| : : : : :  
Db 906 TTLASKCTPLQVWNLNDLYTFDGI 931

## RESULT 23

T22210  
hypothetical protein F44G4.7 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T22210  
R;Sims, M.  
submitted to the EMBL Data Library, June 1995  
A;Reference number: Z19530  
A;Accession: T22210



**RESULT 28**  
GNLJG4  
HIV-1 retropepsin (EC 3.4.23.16) - simian immunodeficiency virus (African green monkey iN; Contains: endonuclease (EC 3.1.1.-); retropepsin (EC 3.4.23.16); RNA-directed DNA poly C; Species: simian immunodeficiency virus, SIV  
C; Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 03-Jun-2002  
C; Accession: B30045  
R; Fukasawa, M.; Miura, T.; Hasegawa, A.; Morikawa, S.; Tsujimoto, H.; Miki, K.; Kitamura Nature 333, 457-461, 1988  
A; Title: Sequence of simian immunodeficiency virus from African green monkey, a new mem A; Reference number: A30045; MUID:88232906; PMID:3374586  
A; Accession: B30045  
A; Molecule type: DNA  
A; Residues: 1-1061 <P>  
A; Cross-references: EMBL:X07805; NID:g61748; PID:g1335593  
C; Comment: Specific enzymatic cleavages may yield mature proteins including protease, re C; Genetics:  
A; Gene: pol  
C; Superfamily: pol polypeptide  
C; Keywords: aspartic proteinase; hydrolase; nucleotidytransferase; polypeptide; reverse F; 11-210/Product: retropepsin #status predicted <RTP>  
F; 134/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 32.7%; Score 48; DB 1; Length 1061;  
Best Local Similarity 52.9%; Pred. No. 95;  
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

**QY** 10 TQLQLEHLLDLQIMLN 26  
|||::|||: |||  
**Db** 976 TQEIQHLQTKIKILN 992

**RESULT 29**  
Tl1685  
hypothetical protein SPBC21D10.13 SPBC1921.07c - fission yeast (Schizosaccharomyces pombe C; Species: Schizosaccharomyces pombe  
C; Date: 16-Jul-1999 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C; Accession: Tl1685; T39791  
R; Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, September 1998  
A; Reference number: Z17313  
A; Accession: Tl1685  
A; Status: preliminary; translated from GB/EMBL/DDBJ  
A; Molecule type: DNA  
A; Residues: 1-155 <SEE>  
A; Cross-references: UNIPROT:Q9USW9; EMBL:AL031536; NID:e1319499  
A; Experimental source: strain 972h(-)  
R; Seeger, K.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, October 1999  
A; Reference number: Z21816  
A; Accession: T39791  
A; Status: preliminary  
A; Molecule type: DNA  
A; Residues: 129-244 <SE2>  
A; Cross-references: EMBL:AL122033; PIDN:CAB58973.1; GSPDB:GM00067; SPDB:SPBC1921.07c C; Genetics:  
A; Map position: IIR  
A; Note: SPBC21D10.13  
A; Note: intron positions not resolved (incomplete sequence)

Query Match 32.3%; Score 47.5; DB 2; Length 244;  
Best Local Similarity 45.8%; Pred. No. 22;  
Matches 11; Conservative 4; Mismatches 6; Indels 3; Gaps 1;

**QY** 3 TSSSTKKTQLQLEHLLDLQIMLN 26  
|||::|||: |||  
**Db** 59 TSEEQKK--ELEHTMQSLEMIIN 79

**RESULT 30**  
F86548  
polymorphic outer membrane protein E family [imported] - Chlamydomophila pneumoniae (strain

RESULT 28  
GNLJG4

HIV-1 retropepsin (EC 3.4.23.16) - simian immunodeficiency virus (African green monkey) N; Contains: endonuclease (EC 3.1.1.-); retropepsin (EC 3.4.23.16); RNA-directed DNA polymerase (EC 2.7.7.49); reverse transcriptase (EC 1.1.1.5); integrase (EC 2.2.1.20); RNase H (EC 3.1.1.7); RNase H2 (EC 3.1.1.13); RNase L (EC 3.1.1.62); RNase M1 (EC 3.1.1.63); RNase M2 (EC 3.1.1.64); RNase M3 (EC 3.1.1.65); RNase M4 (EC 3.1.1.66); RNase M5 (EC 3.1.1.67); RNase M6 (EC 3.1.1.68); RNase M7 (EC 3.1.1.69); RNase M8 (EC 3.1.1.70); RNase M9 (EC 3.1.1.71); RNase M10 (EC 3.1.1.72); RNase M11 (EC 3.1.1.73); RNase M12 (EC 3.1.1.74); RNase M13 (EC 3.1.1.75); RNase M14 (EC 3.1.1.76); RNase M15 (EC 3.1.1.77); RNase M16 (EC 3.1.1.78); RNase M17 (EC 3.1.1.79); RNase M18 (EC 3.1.1.80); RNase M19 (EC 3.1.1.81); RNase M20 (EC 3.1.1.82); RNase M21 (EC 3.1.1.83); RNase M22 (EC 3.1.1.84); RNase M23 (EC 3.1.1.85); RNase M24 (EC 3.1.1.86); RNase M25 (EC 3.1.1.87); RNase M26 (EC 3.1.1.88); RNase M27 (EC 3.1.1.89); RNase M28 (EC 3.1.1.90); RNase M29 (EC 3.1.1.91); RNase M30 (EC 3.1.1.92); RNase M31 (EC 3.1.1.93); RNase M32 (EC 3.1.1.94); RNase M33 (EC 3.1.1.95); RNase M34 (EC 3.1.1.96); RNase M35 (EC 3.1.1.97); RNase M36 (EC 3.1.1.98); RNase M37 (EC 3.1.1.99); RNase M38 (EC 3.1.1.100); RNase M39 (EC 3.1.1.101); RNase M40 (EC 3.1.1.102); RNase M41 (EC 3.1.1.103); RNase M42 (EC 3.1.1.104); RNase M43 (EC 3.1.1.105); RNase M44 (EC 3.1.1.106); RNase M45 (EC 3.1.1.107); RNase M46 (EC 3.1.1.108); RNase M47 (EC 3.1.1.109); RNase M48 (EC 3.1.1.110); RNase M49 (EC 3.1.1.111); RNase M50 (EC 3.1.1.112); RNase M51 (EC 3.1.1.113); RNase M52 (EC 3.1.1.114); RNase M53 (EC 3.1.1.115); RNase M54 (EC 3.1.1.116); RNase M55 (EC 3.1.1.117); RNase M56 (EC 3.1.1.118); RNase M57 (EC 3.1.1.119); RNase M58 (EC 3.1.1.120); RNase M59 (EC 3.1.1.121); RNase M60 (EC 3.1.1.122); RNase M61 (EC 3.1.1.123); RNase M62 (EC 3.1.1.124); RNase M63 (EC 3.1.1.125); RNase M64 (EC 3.1.1.126); RNase M65 (EC 3.1.1.127); RNase M66 (EC 3.1.1.128); RNase M67 (EC 3.1.1.129); RNase M68 (EC 3.1.1.130); RNase M69 (EC 3.1.1.131); RNase M70 (EC 3.1.1.132); RNase M71 (EC 3.1.1.133); RNase M72 (EC 3.1.1.134); RNase M73 (EC 3.1.1.135); RNase M74 (EC 3.1.1.136); RNase M75 (EC 3.1.1.137); RNase M76 (EC 3.1.1.138); RNase M77 (EC 3.1.1.139); RNase M78 (EC 3.1.1.140); RNase M79 (EC 3.1.1.141); RNase M80 (EC 3.1.1.142); RNase M81 (EC 3.1.1.143); RNase M82 (EC 3.1.1.144); RNase M83 (EC 3.1.1.145); RNase M84 (EC 3.1.1.146); RNase M85 (EC 3.1.1.147); RNase M86 (EC 3.1.1.148); RNase M87 (EC 3.1.1.149); RNase M88 (EC 3.1.1.150); RNase M89 (EC 3.1.1.151); RNase M90 (EC 3.1.1.152); RNase M91 (EC 3.1.1.153); RNase M92 (EC 3.1.1.154); RNase M93 (EC 3.1.1.155); RNase M94 (EC 3.1.1.156); RNase M95 (EC 3.1.1.157); RNase M96 (EC 3.1.1.158); RNase M97 (EC 3.1.1.159); RNase M98 (EC 3.1.1.160); RNase M99 (EC 3.1.1.161); RNase M100 (EC 3.1.1.162); RNase M101 (EC 3.1.1.163); RNase M102 (EC 3.1.1.164); RNase M103 (EC 3.1.1.165); RNase M104 (EC 3.1.1.166); RNase M105 (EC 3.1.1.167); RNase M106 (EC 3.1.1.168); RNase M107 (EC 3.1.1.169); RNase M108 (EC 3.1.1.170); RNase M109 (EC 3.1.1.171); RNase M110 (EC 3.1.1.172); RNase M111 (EC 3.1.1.173); RNase M112 (EC 3.1.1.174); RNase M113 (EC 3.1.1.175); RNase M114 (EC 3.1.1.176); RNase M115 (EC 3.1.1.177); RNase M116 (EC 3.1.1.178); RNase M117 (EC 3.1.1.179); RNase M118 (EC 3.1.1.180); RNase M119 (EC 3.1.1.181); RNase M120 (EC 3.1.1.182); RNase M121 (EC 3.1.1.183); RNase M122 (EC 3.1.1.184); RNase M123 (EC 3.1.1.185); RNase M124 (EC 3.1.1.186); RNase M125 (EC 3.1.1.187); RNase M126 (EC 3.1.1.188); RNase M127 (EC 3.1.1.189); RNase M128 (EC 3.1.1.190); RNase M129 (EC 3.1.1.191); RNase M130 (EC 3.1.1.192); RNase M131 (EC 3.1.1.193); RNase M132 (EC 3.1.1.194); RNase M133 (EC 3.1.1.195); RNase M134 (EC 3.1.1.196); RNase M135 (EC 3.1.1.197); RNase M136 (EC 3.1.1.198); RNase M137 (EC 3.1.1.199); RNase M138 (EC 3.1.1.200); RNase M139 (EC 3.1.1.201); RNase M140 (EC 3.1.1.202); RNase M141 (EC 3.1.1.203); RNase M142 (EC 3.1.1.204); RNase M143 (EC 3.1.1.205); RNase M144 (EC 3.1.1.206); RNase M145 (EC 3.1.1.207); RNase M146 (EC 3.1.1.208); RNase M147 (EC 3.1.1.209); RNase M148 (EC 3.1.1.210); RNase M149 (EC 3.1.1.211); RNase M150 (EC 3.1.1.212); RNase M151 (EC 3.1.1.213); RNase M152 (EC 3.1.1.214); RNase M153 (EC 3.1.1.215); RNase M154 (EC 3.1.1.216); RNase M155 (EC 3.1.1.217); RNase M156 (EC 3.1.1.218); RNase M157 (EC 3.1.1.219); RNase M158 (EC 3.1.1.220); RNase M159 (EC 3.1.1.221); RNase M160 (EC 3.1.1.222); RNase M161 (EC 3.1.1.223); RNase M162 (EC 3.1.1.224); RNase M163 (EC 3.1.1.225); RNase M164 (EC 3.1.1.226); RNase M165 (EC 3.1.1.227); RNase M166 (EC 3.1.1.228); RNase M167 (EC 3.1.1.229); RNase M168 (EC 3.1.1.230); RNase M169 (EC 3.1.1.231); RNase M170 (EC 3.1.1.232); RNase M171 (EC 3.1.1.233); RNase M172 (EC 3.1.1.234); RNase M173 (EC 3.1.1.235); RNase M174 (EC 3.1.1.236); RNase M175 (EC 3.1.1.237); RNase M176 (EC 3.1.1.238); RNase M177 (EC 3.1.1.239); RNase M178 (EC 3.1.1.240); RNase M179 (EC 3.1.1.241); RNase M180 (EC 3.1.1.242); RNase M181 (EC 3.1.1.243); RNase M182 (EC 3.1.1.244); RNase M183 (EC 3.1.1.245); RNase M184 (EC 3.1.1.246); RNase M185 (EC 3.1.1.247); RNase M186 (EC 3.1.1.248); RNase M187 (EC 3.1.1.249); RNase M188 (EC 3.1.1.250); RNase M189 (EC 3.1.1.251); RNase M190 (EC 3.1.1.252); RNase M191 (EC 3.1.1.253); RNase M192 (EC 3.1.1.254); RNase M193 (EC 3.1.1.255); RNase M194 (EC 3.1.1.256); RNase M195 (EC 3.1.1.257); RNase M196 (EC 3.1.1.258); RNase M197 (EC 3.1.1.259); RNase M198 (EC 3.1.1.260); RNase M199 (EC 3.1.1.261); RNase M200 (EC 3.1.1.262); RNase M201 (EC 3.1.1.263); RNase M202 (EC 3.1.1.264); RNase M203 (EC 3.1.1.265); RNase M204 (EC 3.1.1.266); RNase M205 (EC 3.1.1.267); RNase M206 (EC 3.1.1.268); RNase M207 (EC 3.1.1.269); RNase M208 (EC 3.1.1.270); RNase M209 (EC 3.1.1.271); RNase M210 (EC 3.1.1.272); RNase M211 (EC 3.1.1.273); RNase M212 (EC 3.1.1.274); RNase M213 (EC 3.1.1.275); RNase M214 (EC 3.1.1.276



R.; Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mwes, H.W.; Mayer, K.  
submitted to the Protein Sequence Database, February 1999  
A:Reference number: Z15420  
A:Accession: T05656  
A:Molecule type: DNA  
A:Residues: 1-159 <BEV>  
A:Cross-references: UNIPROT:Q9SVF7; EMBL:AL035539  
A:Experimental source: cultivar Columbia; BAC clone F22I13  
C:Genetics:  
A:Map position: 4  
A:Introns: 117/1  
A>Note: F22I13.50  
C:Superfamily: Arabidopsis thaliana hypothetical protein F22I13.50

Query Match 31.6%; Score 46.5; DB 2; Length 159;  
Best Local Similarity 46.4%; Pred. No. 19;  
Matches 13; Conservative 3; Mismatches 9; Indels 3; Gaps 1;

Oy 2 PTSSSTKKTQLQLEHLLLDQMILNGIN 29  
||| :| | | | | | | | | | |  
Db 83 PTPTSHK---LDWEERYHLQMLNKLN 107

RESULT 38  
C84888  
hypothetical protein At2g45250 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C:Accession: C84888  
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487; PMID:10617197  
A:Accession: C84888  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-211 <STO>  
A:Cross-references: UNIPROT:O22147; GB:A5002093; NID:g2583136; PIDN:AAB82645.1; GSPDB:GN  
C:Genetics:  
A:Gene: At2g45250  
A:Map position: 2  
C:Superfamily: Arabidopsis thaliana hypothetical protein F22I13.50

Query Match 31.6%; Score 46.5; DB 2; Length 211;  
Best Local Similarity 46.4%; Pred. No. 26;  
Matches 13; Conservative 3; Mismatches 9; Indels 3; Gaps 1;

Oy 2 PTSSSTKKTQLQLEHLLLDQMILNGIN 29  
||| :| | | | | | | | | | |  
Db 117 PTPTSHK---LDWEERYHLQMLNKLN 141

RESULT 39  
A71946  
hypothetical protein jhp0321 - Helicobacter pylori (strain J99)  
C:Species: Helicobacter pylori  
A:Variety: strain J99  
C:Date: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change 09-Jul-2004  
C:Accession: A71946  
R/Ilm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;  
Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;  
Nature 397, 176-180, 1999  
A>Title: Genomic sequence comparison of two unrelated isolates of the human gastric path  
A:Reference number: A71800; MUID:99120557; PMID:9923682  
A:Accession: A71946  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-293 <ARN>  
A:Cross-references: UNIPROT:Q9ZMA1; GB:A5001468; GB:A5001439; NID:g4154838; PIDN:AAD0059T  
A:Experimental source: strain J99  
C:Genetics:

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 23, 2005, 12:39:59 ; Search time 52.8525 Seconds  
(without alignments)  
300.354 Million cell updates/sec

Title: US-10-727-514-2

Perfect score: 152

Sequence: 1 MAPTSSSTKTKQLQLEHLILDQMLINGINN 31

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	147	96.7	150	2 Q9C001	Q9C001 homo sapien
2	147	96.7	153	1 IL2 HUMAN	P60568 homo sapien
3	147	96.7	153	1 IL2_HYLLA	P60569 hylobates l
4	147	96.7	153	2 Q6NZ93	Q6NZ93 homo sapien
5	147	96.7	154	1 IL2_MACFA	Q29615 macaca fasc
6	147	96.7	154	1 IL2_MACMU	P68291 macaca mulla
7	147	96.7	154	1 IL2_MACNE	P68290 macaca neme
8	147	96.7	154	1 IL2_PAPAN	Q865Y1 papio anubi
9	145	95.4	154	1 IL2_SAISC	Q8mKh2 salmirl sci
10	145	95.4	154	2 Q7JFM2	Q7Jfm2 aotus lemur
11	145	95.4	154	2 Q7JFM3	Q7Jfm3 aotus nigri
12	145	95.4	154	2 Q7JFM4	Q7Jfm4 aotus vocif
13	145	95.4	154	2 Q7JFM5	Q7Jfm5 aotus nancy
14	145	95.4	154	2 Q9XS38	Q9Xe38 papio hamad
15	143	94.1	133	2 Q6QWNO	Q6Qwn0 homo sapien
16	143	94.1	133	2 Q727M3	Q727m3 homo sapien
17	142	93.4	154	1 IL2_CERTO	P46649 cercocebus
18	137	90.1	153	2 Q6NZ91	Q6nz91 homo sapien
19	135.5	89.1	156	2 Q13169	Q13169 homo sapien
20	134	88.2	139	2 Q16334	Q16334 homo sapien
21	116	76.3	154	1 IL2_MIRAN	Q62641 mirounga an
22	114	75.0	154	1 IL2_FELCA	Q07885 felis silve
23	108.5	71.4	155	2 Q9XT83	Q9xc83 halichoerus
24	107.5	70.7	66	2 Q9BG74	Q9Bg74 canis fami
25	107.5	70.7	155	1 IL2_CANFA	Q29416 canis fami
26	107	70.4	79	2 Q9TV12	Q9tv12 canis fami
27	107	70.4	152	2 Q80XG3	Q80xg3 peromyscus
28	107	70.4	153	1 IL2_RABIT	Q77620 coryctolagus
29	106	69.7	133	2 Q9MZR9	Q9mzr9 coryctolagus
30	106	69.7	155	2 Q923T2	Q923t2 sigmodon hi
31	103	67.8	138	2 Q70329	Q70329 mesocricetu

32	97	63.8	155	1	IL2_RAT	P17108 rattus norv
33	96	63.2	154	1	IL2_PIG	P26891 sus scrofa
34	95	62.5	155	1	IL2_MERUN	Q08081 meriones un
35	93	61.2	154	2	Q865X2	Q865x2 lama glama
36	92	60.5	149	1	IL2_HORSE	P37997 equus cabal
37	91	59.9	23	2	Q9UCF5	Q9ucf5 homo sapien
38	88	57.9	152	1	IL2_ORCOR	Q97513 orcinus orc
39	87	57.2	38	2	Q71V48	Q71v48 homo sapien
40	83	54.6	154	2	Q9XT84	Q9xt84 delphinapte
41	82	53.9	152	2	Q88210	Q88210 cavia porce
42	79	52.0	69	2	Q9GJRA	Q9gjr4 ovia aries
43	79	52.0	136	2	Q8E220	Q8e220 capra hircu
44	79	52.0	145	2	Q8HZ67	Q8hz67 bos indicus
45	79	52.0	155	1	IL2_BOVIN	P05016 bos taurus
46	79	52.0	155	1	IL2_BUBBU	Q95kp3 bubalus bub
47	79	52.0	155	1	IL2_CAPHI	P36835 capra hircu
48	79	52.0	155	1	IL2_SHEEP	P19114 ovia aries
49	79	52.0	155	2	Q8HYR7	Q8hyr7 bos taurus
50	79	52.0	155	2	Q9GL83	Q9gl83 capra hircu
51	79	52.0	162	1	IL2_CEREL	P51747 cervus elap
52	77	50.7	147	2	Q7YRQ2	Q7yrr2 bos mutus g
53	69	45.4	39	2	Q9BG73	Q9bg73 canis fami
54	69	45.4	150	2	P70291	P70291 mus musculu
55	69	45.4	169	2	Q9QUS8	Q9qus8 mus musculu
56	67	44.1	150	2	P70294	P70294 mus musculu
57	65.5	43.1	155	2	P70292	P70292 mus musculu
58	64.5	42.4	166	1	IL2_MUSSP	Q08867 mus sprētus
59	64	42.1	63	2	Q8BHA4	Q8bha4 mus musculu
60	64	42.1	155	2	Q85QE7	Q85qe7 nanheimia
61	64	42.1	169	1	IL2_MOUSE	P04351 mus musculu
62	62.5	41.1	159	2	P70293	P70293 mus musculu
63	54	35.5	304	2	Q841X8	Q841x8 campylobact
64	54	35.5	357	1	AAAA_EMENI	P21133 emericeella
65	52	34.2	101	2	Q6DUY6	Q6duy6 cryptospori
66	52	34.2	116	2	Q29138	Q29138 trichospori
67	52	34.2	155	1	YHCH_HAEIN	P44583 haemophilus
68	52	34.2	285	2	Q83F57	Q83f57 coxiella bu
69	52	34.2	300	2	Q8VW37	Q8vw37 coxiella bu
70	52	34.2	300	2	Q841J1	Q841j1 coxiella bu
71	52	34.2	300	2	Q841J2	Q841j2 coxiella bu
72	52	34.2	737	2	Q8KTG5	Q8ktg5 vibrio chol
73	52	34.2	746	2	Q8FNH5	Q8fnh5 candida gla
74	52	34.2	1530	2	Q81BS2	Q81bs2 plasmodium
75	51.5	33.9	2673	2	Q7QPT6	Q7qpt6 giardia lam
76	51	33.6	95	2	Q8BN23	Q8bn23 mus musculu
77	51	33.6	304	2	Q930K5	Q930k5 rhizobium m
78	51	33.6	322	2	Q72UY1	Q72uy1 leptospira
79	51	33.6	322	2	Q8EZZ2	Q8ezz2 leptospira
80	51	33.6	334	2	Q7NRQ8	Q7nrq8 chromobacte
81	51	33.6	457	2	Q9NIP5	Q9nip5 strongyloce
82	51	33.6	517	2	Q8R6R8	Q8r6r8 thermaoae
83	51	33.6	627	1	FLGK_BORBU	P70859 borrelia bu
84	51	33.6	627	2	Q862I3	Q862i3 borrelia ga
85	50	32.9	193	2	Q7X1Z0	Q7x1z0 oryza sativ
86	50	32.9	365	2	P71599	P71599 mycobacteri
87	50	32.9	365	2	Q7U2Z7	Q7u2z7 mycobacteri
88	50	32.9	651	2	Q8OUN2	Q8oun2 mus musculu
89	50	32.9	703	2	Q68WE5	Q68we5 rickettsia
90	50	32.9	749	2	Q7TQEI	Q7tqe1 mus musculu
91	50	32.9	767	2	Q6PKB8	Q6pkb8 homo sapien
92	50	32.9	769	2	Q6KAM1	Q6kam1 mus musculu
93	50	32.9	788	1	PCAP_HUMAN	Q94rn5 homo sapien
94	50	32.9	792	1	PCAP_MOUSE	Q94rh2 mus musculu
95	50	32.9	1046	1	POL_SIVAG	P27980 sinian immu
96	50	32.9	1454	1	CSF2_HUMAN	Q60244 h cofactor
97	50	32.9	1476	2	Q6FJ05	Q6fj05 candida gla
98	50	32.9	3175	1	RFOA_EAV	P19811 equine arte
99	49.5	32.6	715	2	Q8EJ30	Q8ej30 shewanella
100	49.5	32.6	1518	2	Q7RA10	Q7ra10 plasmodium

ALIGNMENTS

```

RESULT 1
Q9C001 ID Q9C001 PRELIMINARY; PRT; 150 AA.
AC Q9C001;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interleukin-2 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=20545237; PubMed=11093171;
RX DOI=10.1002/1521-4141(2000012)30:12<3516::AID-IMMU3516>3.0.CO;2-S;
RA Mateanz F., Delgado C., Fresno M., Alcina A.;
RT "Allelic selection of human IL-2 gene.";
RL Eur. J. Immunol. 30:3516-3521(2000).
DR EMBL; AF228636; AAG53575.1; -.
DR HSP; P60568; IIRL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:000134; F:interleukin-2 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
DR NON_TER 150 150
SQ SEQUENCE 150 AA; 17312 MW; BF5860F8436ACE5 CRC64;

Query Match 96.7%; Score 147; DB 2; Length 150;
Best Local Similarity 100.0%; Pred. No. 8.5e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKTQLQLEHLLDLQMLINGINN 31
Db |||||
21 APTSSSTKTQLQLEHLLDLQMLINGINN 50

RESULT 2
IL2_HUMAN IL2_HUMAN STANDARD; PRT; 153 AA.
AC P60568; P01585;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF)
DE (Algesleukin).
GN Name=IL2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=84247353; PubMed=6330695;
RA Holbrook N.J., Lieber M., Crabtree G.R.;
RT "DNA sequence of the 5' flanking region of the human interleukin 2
gene: homologues with adult T-cell leukemia virus.";
RL Nucleic Acids Res. 12:5005-5013(1984).
RN [2]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=83167472; PubMed=6403867;
RA Taniguchi T., Matsui H., Fujita T., Takaoka C., Kashima N.,
RA Yoshimoto K., Hamuro J.;
RT "Structure and expression of a cloned cDNA for human interleukin-2.";
RL Nature 302:305-310(1983).
RN [3]_TaxID=9606;

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RP SEQUENCE FROM N.A.
RX MEDLINE=84023840; PubMed=6312994;
RA Maeda S., Nishino N., Obaru K., Mita S., Nomiya H., Shimada K.,
RA Fujimoto K., Teranishi T., Hirano T., Onoue K.;
RT "Cloning of interleukin 2 mRNAs from human tonsils.";
RL Biochem. Biophys. Res. Commun. 115:1040-1047(1983).
RN [4]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=83246551; PubMed=6306584;
RA Devos R., Plaetnick G., Cheroutre H., Simons G., Degraeve W.,
RA Tavernier J., Remaut E., Fiers W.;
RT "Molecular cloning of human interleukin 2 cDNA and its expression in
E. coli.";
RL Nucleic Acids Res. 11:4307-4323(1983).
RN [5]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=84170356; PubMed=6608729;
RA Holbrook N.J., Smith K.A., Fornace A.J. Jr., Comeau C.M.,
RA Wiskocil R.L., Crabtree G.R.;
RT "T-cell growth factor: complete nucleotide sequence and organization
of the gene in normal and malignant cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:1634-1638(1984).
RN [6]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=84170243; PubMed=6324170;
RA Fujita T., Takaoka C., Matsui H., Taniguchi T.;
RT "Structure of the human interleukin 2 gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:7437-7441(1983).
RN [7]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=95239150; PubMed=7722480;
RA Eisenberg O., Faber-Elman A., Lotan M., Schwartz M.;
RT "Interleukin-2 transcripts in human and rodent brains: possible
expression by astrocytes.";
RL J. Neurochem. 64:1928-1936(1995).
RN [8]_TaxID=9606;
RP SEQUENCE FROM N.A.
RX MEDLINE=96422299; PubMed=8824916;
DOI=10.1002/(SICI)1098-2795(199602)43:2<180::AID-MRD7>3.3.CO;2-D;
RA Chernicky C.L., Tan H., Burfeind P., Ilan J., Ilan J.;
RT "Sequence of interleukin-2 isolated from human placental poly A+ RNA:
possible role in maintenance of fetal allograft.";
RL Mol. Reprod. Dev. 43:180-186(1996).
RN [9]_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RT "SeattleSNPs: NHLBI HL66682 program for genomic applications, UW-
PHRCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [10]_TaxID=9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S., Krzywinski M.I., Skalska U., Smalls D.B.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

```



RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [11]  
 RP SEQUENCE OF 21-153 FROM N.A.  
 RX MEDLINE=89062420; PubMed=3264184;  
 RA Weir M.P., Chaplin M.A., Wallace D.M., Dykes C.W., Hobden A.N.;  
 RT "Structure-activity relationships of recombinant human interleukin  
 2.";  
 RL Biochemistry 27:6883-6892(1988).  
 RN [12]  
 RP SEQUENCE OF 1-69 FROM N.A.  
 RX MEDLINE=87064618; PubMed=3491296;  
 RA Siebenlist U., Durand D.B., Bressler P., Holbrook N.J., Norris C.A.,  
 RA Kamoun M., Kant J.A., Crabtree G.R.;  
 RT "Promoter region of interleukin-2 gene undergoes chromatin structure  
 changes and confers inducibility on chloramphenicol acetyltransferase  
 gene during activation of T cells.";  
 RL Mol. Cell. Biol. 6:3042-3049(1986).  
 RN [13]  
 RP SEQUENCE OF 1-68 FROM N.A.  
 RA Nishino N., Obaru K., Maeda S., Shimada K., Onoue K.;  
 RT "Organization of the DNA regions flanking the human interleukin 2  
 gene.";  
 RL Biomed. Res. 6:197-205(1985).  
 RN [14]  
 RP SEQUENCE OF 21-153, DISULFIDE BOND, AND CARBOHYDRATE-LINKAGE SITE.  
 RX MEDLINE=85038540; PubMed=6333684;  
 RA Robb R.J., Kutny R.M., Panico M., Morris H.R., Chowdhry V.;  
 RT "Amino acid sequence and post-translational modification of human  
 interleukin 2.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 81:6486-6490(1984).  
 RN [15]  
 RP CARBOHYDRATE-LINKAGE SITE.  
 RX MEDLINE=90008901; PubMed=2793860;  
 RA Conradt H.S., Nimz M., Dittmar K.E.J., Lindenmaier W., Hoppe J.,  
 RA Hauser H.;  
 RT "Expression of human interleukin-2 in recombinant baby hamster kidney,  
 Ltk-, and Chinese hamster ovary cells. Structure of O-linked  
 carbohydrate chains and their location within the polypeptide.";  
 RL J. Biol. Chem. 264:17368-17373(1989).  
 RN [16]  
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).  
 RX MEDLINE=88070646; PubMed=3500515;  
 RA Brandhuber B.J., Boone T., Kenney W.C., McKay D.B.;  
 RT "Three-dimensional structure of interleukin-2.";  
 RL Science 238:1707-1709(1987).  
 RN [17]  
 RP COMPARISON OF X-RAY STRUCTURES.  
 RX MEDLINE=92335891; PubMed=1631562;  
 RA Bazan J.F.;  
 RT "Unravelling the structure of IL-2.";  
 RL Science 257:410-412(1992).  
 RN [18]  
 RP RESPONSE TO ABOVE LETTER.  
 RX McKay D.B.;  
 RA Science 257:412-413(1992).  
 RN [19]  
 RP STRUCTURE BY NMR.  
 RX MEDLINE=92379010; PubMed=1510960;  
 RA Mott H.R., Driscoll P.C., Boyd J., Cooke R.M., Weir M.P.,  
 RA Campbell I.D.;  
 RT "Secondary structure of human interleukin 2 from 3D heteronuclear NMR  
 experiments.";  
 RL Biochemistry 31:7741-7744(1992).  
 RN [20]  
 RP 3D-STRUCTURE MODELING.  
 RX MEDLINE=95111955; PubMed=7529123;  
 RA Bamrough P., Hedgecock C.J., Richards W.G.;  
 RT "The interleukin-2 and interleukin-4 receptors studied by molecular  
 modelling.";  
 RL Structure 2:839-851(1994).  
 CC -!- FUNCTION: Produced by T-cells in response to antigenic or  
 mitogenic stimulation, this protein is required for T-cell

proliferation and other activities crucial to regulation of the  
 immune response. Can stimulate B cells, monocytes, lymphokine-  
 activated killer cells, natural killer cells, and glioma cells.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- DISEASE: Involved in a form of T-cell acute lymphoblastic leukemia  
 (T-ALL) by a chromosomal translocation t(4;16)(q26;p13) which  
 involves TNFRSF17 and IL2.  
 CC -!- PHARMACEUTICAL: Available under the name Proleukin (Chiron). Used  
 in patients with renal cell carcinoma or metastatic melanoma.  
 CC -!- SIMILARITY: Belongs to the IL-2 family.  
 CC -!- DATABASE: NAME=RD Systems' cytokine source book: IL2;  
 WWW="http://www.rndsystems.com/asp/g\_sitebuilder.asp?bodyid=206".  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 or send an email to license@isb-sib.ch).  
 CC  
 CC EMBL; J00264; A048509.1; -;  
 DR EMBL; X01586; CAA25742.1; -;  
 DR EMBL; V00564; CAA23827.1; -;  
 DR EMBL; X00695; CAA25292.1; -;  
 DR EMBL; K02056; AAA98792.1; -;  
 DR EMBL; M13879; AAA59141.1; -;  
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 Best Local Similarity 100.0%; Pred. No. 8.7e-14;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 APTSSSTKTQLQLEHLLDLQMLNGINN 31  
 DB 21 APTSSSTKTQLQLEHLLDLQMLNGINN 50  
 RESULT 3  
 IL2\_HYLLA  
 ID IL2\_HYLLA STANDARD; PRT; 153 AA.  
 AC P60569; P01585;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).  
 GN Name=IL2;  
 OS Hylobates lar (Common gibbon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.  
 OX NCBI\_TaxID=9580;  
 RN [1]\_TaxID=9580;  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=86042650; PubMed=3877307;  
 RA Chen S.J., Holbrook N.J., Mitchell K.F., Vallone C.A., Greengard J.S.,  
 RA Crabtree G.R., Lin Y.;  
 RT "A viral long terminal repeat in the interleukin 2 gene of a cell line  
 that constitutively produces interleukin 2.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:7284-7288(1985).  
 CC -!- FUNCTION: Produced by T-cells in response to antigenic or  
 mitogenic stimulation, this protein is required for T-cell  
 proliferation and other activities crucial to regulation of the  
 immune response. Can stimulate B cells, monocytes, lymphokine-  
 activated killer cells, natural killer cells, and glioma cells.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the IL-2 family.  
 CC  
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CC -----
DR EMBL; M11144; AAA35454.1; -.
DR PIR; A94067; ICG12.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR ProDom; PD003649; Interleukin-2.
DR PRINTS; PR00265; INTERLEUKIN2.
DR SMART; SM00189; IL2; 1.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN 2; 1.
DR Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
KW T-cell.
FT SIGNAL 1 20 By similarity.
FT CHAIN 21 153 Interleukin-2.
FT CARBOHYD 23 23 O-linked (GalNac. . .) (By similarity).
FT DISULFID 78 125 By similarity.
SQ SEQUENCE 153 AA; 17628 MW; 59E2F40F25860F84 CRC64;

Query Match 96.7%; Score 147; DB 1; Length 153;
Best Local Similarity 100.0%; Pred. No. 8.7e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLLDQMILNGINN 31
DB 21 APTSSSTKKTQLEHLLLDQMILNGINN 50

RESULT 4
Q6N293 PRELIMINARY; PRT; 153 AA.
ID Q6N293
AC Q6N293;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Interleukin 2.
GN Name=il2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins E.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinaki M.I., Skalska U., Schmitt J., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RA Strausberg R.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC066254; AAH66254.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.

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DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN 2; 1.
DR SEQUENCE 153 AA; 17597 MW; 1942F50F25960E88 CRC64;

Query Match 96.7%; Score 147; DB 2; Length 153;
Best Local Similarity 100.0%; Pred. No. 8.7e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLLDQMILNGINN 31
DB 21 APTSSSTKKTQLEHLLLDQMILNGINN 50

RESULT 5
IL2_MACFA STANDARD; PRT; 154 AA.
ID IL2_MACFA
AC Q29615;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN Name=il2;
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA Yabe M., Matsuura Y., Tatsumi M.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Produced by T-cells in response to antigenic or
CC mitogenic stimulation, this protein is required for T-cell
CC proliferation and other activities crucial to regulation of the
CC immune response. Can stimulate B cells, monocytes, lymphokine-
CC activated killer cells, natural killer cells, and glioma cells (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-2 family.
CC
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CC or send an email to license@ebi.ac.uk).
CC
CC EMBL; D63352; BAA09676.1; -.
DR HSSP; P01585; 1M49.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN 2; 1.
KW Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
T-cell.
FT SIGNAL 1 20 By similarity.
FT CHAIN 21 154 Interleukin-2.
FT CARBOHYD 23 23 O-linked (GalNac. . .) (By similarity).
FT DISULFID 78 126 By similarity.
SQ SEQUENCE 154 AA; 17686 MW; 7853FE624A5E4A49 CRC64;

Query Match 96.7%; Score 147; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 8.8e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2 APTSSSTKKTQLQLEHLLDLQMLNGINN 31
DB 21 APTSSSTKKTQLQLEHLLDLQMLNGINN 50

RESULT 6
IL2_MACMU STANDARD; PRT; 154 AA.
AC P68290; P51498;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN Name=IL2;
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
nonhuman primates.";
RL J. Immunol. 155:3946-3954(1995).
CC -!- FUNCTION: Produced by T-cells in response to antigenic or
mitogenic stimulation, this protein is required for T-cell
proliferation and other activities crucial to regulation of the
immune response. Can stimulate B cells, monocytes, lymphokine-
activated killer cells, natural killer cells, and glioma cells (By
similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-2 family.
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CC -----
CC EMBL; U19847; AAB60400.1; -.
CC HSP; P01585; IMA8.
CC InterPro; IPR009079; 4_helix_cytokine.
CC InterPro; IPR000779; Interleukin-2.
CC Pfam; PF00715; IL2; 1.
CC PRINTS; PR00265; INTERLEUKIN2.
CC SMART; SM00189; IL2; 1.
CC PROSITE; PS00424; INTERLEUKIN_2; 1.
CC Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
KW T-cell.
FT SIGNAL 1 20 By similarity.
FT CHAIN 21 154 Interleukin-2.
FT CARBOHYD 23 23 O-linked (GalNAc...) (By similarity).
FT DISULFID 78 126 By similarity.
SQ SEQUENCE 154 AA; 17685 MW; 6AEEA480F204BA49 CRC64;

Query Match 96.7%; Score 147; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 8.8e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLLDLQMLNGINN 31
DB 21 APTSSSTKKTQLQLEHLLDLQMLNGINN 50

RESULT 7
IL2_MACNE STANDARD; PRT; 154 AA.
AC P68290; P51498;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN Name=IL2;
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
nonhuman primates.";
RL J. Immunol. 155:3946-3954(1995).
CC -!- FUNCTION: Produced by T-cells in response to antigenic or
mitogenic stimulation, this protein is required for T-cell
proliferation and other activities crucial to regulation of the
immune response. Can stimulate B cells, monocytes, lymphokine-
activated killer cells, natural killer cells, and glioma cells (By
similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-2 family.
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CC -----
CC EMBL; U19847; AAB60400.1; -.
CC HSP; P01585; IMA8.
CC InterPro; IPR009079; 4_helix_cytokine.
CC InterPro; IPR000779; Interleukin-2.
CC Pfam; PF00715; IL2; 1.
CC PRINTS; PR00265; INTERLEUKIN2.
CC SMART; SM00189; IL2; 1.
CC PROSITE; PS00424; INTERLEUKIN_2; 1.
CC Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
KW T-cell.
FT SIGNAL 1 20 By similarity.
FT CHAIN 21 154 Interleukin-2.
FT CARBOHYD 23 23 O-linked (GalNAc...) (By similarity).
FT DISULFID 78 126 By similarity.
SQ SEQUENCE 154 AA; 17685 MW; 6AEEA480F204BA49 CRC64;

Query Match 96.7%; Score 147; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 8.8e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLLDLQMLNGINN 31
DB 21 APTSSSTKKTQLQLEHLLDLQMLNGINN 50

RESULT 8
IL2_PAPAN STANDARD; PRT; 154 AA.
AC Q865Y1;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN Name=IL2; Synonyms=IL-2;
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;

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OC Cercopithecinae; Papio.  
 OX NCBI\_TaxID=9555;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Villinger F.;  
 RT "Nonhuman primate cytokines.";  
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Produced by T-cells in response to antigenic or  
 CC mitogenic stimulation, this protein is required for T-cell  
 CC proliferation and other activities crucial to regulation of the  
 CC immune response. Can stimulate B cells, monocytes, lymphokine-  
 CC activated killer cells, natural killer cells, and glioma cells (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the IL-2 family.  
 CC  
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 CC  
 CC EMBL; AY234220; AAO85333.1; -.  
 DR HSP; P01585; IMA9.  
 DR InterPro; IPR009079; 4 helix cytokine.  
 DR InterPro; IPR000779; Interleukin-2.  
 DR Pfam; PF00715; IL2; 1.  
 DR PRINTS; PR00265; INTERLEUKIN2.  
 DR ProDom; PD003649; Interleukin-2; 1.  
 DR SMART; SM00189; IL2; 1.  
 DR PROSITE; PS00424; INTERLEUKIN 2; 1.  
 DR Cytokine; Glycoprotein; Growth factor; Immune response; Signal;  
 KW T-cell.  
 FT SIGNAL 1 20 By similarity.  
 FT CHAIN 21 154 Interleukin-2.  
 FT DISULFID 78 126 By similarity.  
 FT CARBOHYD 23 23 O-linked (GalNAc...) (By similarity).  
 SQ SEQUENCE 154 AA; 17713 MW; 47F486BDF204AD6E CRC64;  
 Query Match 96.7%; Score 147; DB 1; Length 154;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-14; Mismatches 0; Indels 0; Gaps 0;  
 Matches 30; Conservative 0;  
 QY 2 APTSSSTKTKTQLQLHLLLDLQMLINGINN 31  
 Db 21 APTSSSTKTKTQLQLHLLLDLQMLINGINN 50  
 RESULT 9  
 IL2\_SAISC  
 ID IL2\_SAISC STANDARD; PRT; 154 AA.  
 AC Q8MKH2;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).  
 GN Name=IL2;  
 OS Saimiri sciureus (Common squirrel monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Saimiri.  
 OX NCBI\_TaxID=9521;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21972723; PubMed=11976788; DOI=10.1007/s00251-002-0443-Y;  
 RA Heraud J.M., Lavergne A., Kazanji M.;  
 RT "Molecular cloning, characterization, and quantification of squirrel  
 RT monkey (Saimiri sciureus) Th1 and Th2 cytokines.";  
 RL Immunogenetics 54:120-29(2002).  
 CC -!- FUNCTION: Produced by T-cells in response to antigenic or  
 CC mitogenic stimulation, this protein is required for T-cell  
 CC proliferation and other activities crucial to regulation of the

CC immune response. Can stimulate B cells, monocytes, lymphokine-  
 CC activated killer cells, natural killer cells, and glioma cells (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the IL-2 family.  
 CC  
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 CC  
 CC EMBL; AF294755; AAK92042.1; -.  
 DR HSP; P01585; IMA9.  
 DR InterPro; IPR009079; 4 helix cytokine.  
 DR InterPro; IPR000779; Interleukin-2.  
 DR Pfam; PF00715; IL2; 1.  
 DR PRINTS; PR00265; INTERLEUKIN2.  
 DR ProDom; PD003649; Interleukin-2; 1.  
 DR SMART; SM00189; IL2; 1.  
 DR PROSITE; PS00424; INTERLEUKIN 2; 1.  
 DR Cytokine; Glycoprotein; Growth factor; Immune response; Signal;  
 KW T-cell.  
 FT SIGNAL 1 20 By similarity.  
 FT CHAIN 21 154 Interleukin-2.  
 FT DISULFID 78 126 By similarity.  
 FT CARBOHYD 23 23 O-linked (GalNAc...) (By similarity).  
 SQ SEQUENCE 154 AA; 17657 MW; AA642BABCAS7569 CRC64;  
 Query Match 95.4%; Score 145; DB 1; Length 154;  
 Best Local Similarity 96.7%; Pred. No. 1.8e-13; Mismatches 1; Indels 0; Gaps 0;  
 Matches 29; Conservative 1;  
 QY 2 APTSSSTKTKTQLQLHLLLDLQMLINGINN 31  
 Db 21 APTSSSTKTKTQLQLHLLLDLQMLINGINN 50  
 RESULT 10  
 Q7JFM2  
 ID Q7JFM2 PRELIMINARY; PRT; 154 AA.  
 AC Q7JFM2;  
 DT 05-JUL-2004 (TReMBLrel. 27, Created)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
 DE IL-2.  
 OS Aotus lemurinus (Northern gray-necked night monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotus.  
 OX NCBI\_TaxID=43147;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A.,  
 RA Patarroyo M.E.;  
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U88364; AAD41534.1; -.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005134; F:Interleukin-2 receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR009079; 4 helix\_cytokine.  
 DR InterPro; IPR000779; Interleukin-2.  
 DR Pfam; PF00715; IL2; 1.  
 DR PRINTS; PR00265; INTERLEUKIN2.  
 DR ProDom; PD003649; Interleukin-2; 1.  
 DR SMART; SM00189; IL2; 1.  
 DR PROSITE; PS00424; INTERLEUKIN 2; 1.  
 SQ SEQUENCE 154 AA; 17675 MW; AB752ABBADA96469 CRC64;  
 Query Match 95.4%; Score 145; DB 2; Length 154;  
 Best Local Similarity 96.7%; Pred. No. 1.8e-13; Mismatches 1; Indels 0; Gaps 0;  
 Matches 29; Conservative 1;

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QY 2 APTSSSTKKTQLEHLLDLQMLNGINN 31
Db 21 APTSSSTKKTQLEHLLDLQMLNGINN 50

RESULT 11
Q7JFM3
ID Q7JFM3 PRELIMINARY; PRT; 154 AA.
AC Q7JFM3;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE IL-2.
OS Aotus nigriceps (Black-headed owl monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57175;
RN [1]
RP SEQUENCE FROM N.A.
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A.,
RA Patarrovo M.E.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88363; AAD41536.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005134; P:interleukin-2 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 154 AA, 17675 MW, AB752ABBADA96469 CRC64;

Query Match 95.4%; Score 145; DB 2; Length 154;
Best Local Similarity 96.7%; Pred. No. 1.8e-13;
Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLDLQMLNGINN 31
Db 21 APTSSSTKKTQLEHLLDLQMLNGINN 50

RESULT 12
Q7JFM4
ID Q7JFM4 PRELIMINARY; PRT; 154 AA.
AC Q7JFM4;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE IL-2.
OS Aotus vociferans (Spix's owl monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=57176;
RN [1]
RP SEQUENCE FROM N.A.
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A.,
RA Patarrovo M.E.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88362; AAD41537.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005134; P:interleukin-2 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 154 AA, 17675 MW, AB752ABBADA96469 CRC64;

Query Match 95.4%; Score 145; DB 2; Length 154;
Best Local Similarity 96.7%; Pred. No. 1.8e-13;
Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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SQ SEQUENCE 154 AA, 17675 MW, AB752ABBADA96469 CRC64;

Query Match 95.4%; Score 145; DB 2; Length 154;
Best Local Similarity 96.7%; Pred. No. 1.8e-13;
Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLDLQMLNGINN 31
Db 21 APTSSSTKKTQLEHLLDLQMLNGINN 50

RESULT 13
Q7JFM5
ID Q7JFM5 PRELIMINARY; PRT; 154 AA.
AC Q7JFM5;
DT 05-JUL-2004 (TREMELrel. 27, Created)
DT 05-JUL-2004 (TREMELrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMELrel. 27, Last annotation update)
DE IL-2.
OS Aotus nancymae (Ma's night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
OX NCBI_TaxID=37293;
RN [1]
RP SEQUENCE FROM N.A.
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A.,
RA Patarrovo M.E.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88361; AAD41535.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005134; P:interleukin-2 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 154 AA, 17675 MW, AB752ABBADA96469 CRC64;

Query Match 95.4%; Score 145; DB 2; Length 154;
Best Local Similarity 96.7%; Pred. No. 1.8e-13;
Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLDLQMLNGINN 31
Db 21 APTSSSTKKTQLEHLLDLQMLNGINN 50

RESULT 14
Q9XS38
ID Q9XS38 PRELIMINARY; PRT; 154 AA.
AC Q9XS38;
DT 01-NOV-1999 (TREMELrel. 12, Created)
DT 01-NOV-1999 (TREMELrel. 12, Last sequence update)
DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)
DE IL-2.
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=95557;
RN [1]
RP SEQUENCE FROM N.A.
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A.,
RA Patarrovo M.E.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88365; AAD41538.1; -.
DR HSP; P60568; IIRL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005134; P:interleukin-2 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.

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DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN 2; 1.
SQ SEQUENCE 154 AA; 17675 MW; AB752ABBADA96469 CRC64;

Query Match          95.4%; Score 145; DB 2; Length 154;
Best Local Similarity 96.7%; Pred. No. 1.8e-13;
Matches 29; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLLDLQWLINGINN 31
DB 21 APTSSSTKKTQLQLEHLLDLQWLINGINN 50

RESULT 15
Q6QWNO PRELIMINARY; PRT; 133 AA.
AC Q6QWNO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Interleukin-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN RP SEQUENCE FROM N.A.
RA Chikara S.K., Sharma G.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY23040; AAS1753.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN 2; 1.
SQ SEQUENCE 133 AA; 15462 MW; 1699F680A09DB3B0 CRC64;

Query Match          94.1%; Score 143; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 3e-13;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PTSSSTKKTQLQLEHLLDLQWLINGINN 31
DB 2 PTSSSTKKTQLQLEHLLDLQWLINGINN 30

RESULT 16
Q7Z7M3 PRELIMINARY; PRT; 133 AA.
AC Q7Z7M3;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interleukin-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN RP SEQUENCE FROM N.A.
RA Chikara S.K., Jaiswal P., Sharma G.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY283686; AAP35033.1; -.

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DR HSSP; P60568; 1IRL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005134; F:interleukin-2 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN 2; 1.
SQ SEQUENCE 133 AA; 15461 MW; 1699F6A880959B90 CRC64;

Query Match          94.1%; Score 143; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 3e-13;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PTSSSTKKTQLQLEHLLDLQWLINGINN 31
DB 2 PTSSSTKKTQLQLEHLLDLQWLINGINN 30

RESULT 17
IL2_CERTO STANDARD; PRT; 154 AA.
AC P46649;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN Name=IL2;
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9531;
[1]
RN RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and nonhuman primates.";
RL J. Immunol. 155:3946-3954 (1995).
CC -!- FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokine-activated killer cells, natural killer cells, and glioma cells.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-2 family.
CC
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CC
CC EMBL; U19846; AAB60399.1; -.
DR HSSP; P01585; 1M47.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN 2; 1.
KW Cytokine; Glycoprotein; Growth factor; Immune response; Signal; T-cell.
KW SIGNAL.
FT CHAIN 1 20 By similarity.
FT CHAIN 21 154 Interleukin-2.
FT CARBOHYD 23 23 O-linked (GalNAc... ) (By similarity).

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FT DISULFID 78 126 By similarity.  
 FT VARIANT 25 25 R -> S.  
 FT VARIANT 74 74 K -> E.  
 SQ SEQUENCE 154 AA; 17754 MW; 9F851814204BA48 CRC64;

Query Match 93.4%; Score 142; DB 1; Length 154;  
 Best Local Similarity 96.7%; Pred. No. 4.9e-13;  
 Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKTKTQLEHLLDLQMLINGINN 31  
 DB 21 APTSSSTKTKTQLEHLLDLQMLINGINN 50

RESULT 18  
 Q6NZ91  
 ID Q6NZ91 PRELIMINARY; PRT; 153 AA.  
 AC Q6NZ91;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE Interleukin 2,  
 GN Name=IL2;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PCR rescued clones;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zesberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M.J., Udwin T.B., Toshitoki S., Carninci P., Prange C.,  
 RA Brownstein M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gnaratan P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos J., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PCR rescued clones;  
 RA Strausberg R.;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC066256; AAH66256.1; -;  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005134; F:interleukin-2 receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPRO00779; 4\_helix cytokine.  
 DR InterPro; IPRO00779; Interleukin-2.  
 DR Pfam; PF00715; IL2; 1.  
 DR PRINTS; PR00265; INTERLEUKIN2.  
 DR ProDom; PD003649; Interleukin-2; 1.  
 DR SMART; SM00189; IL2; 1.  
 DR PROSITE; PS00424; INTERLEUKIN 2; 1.  
 SQ SEQUENCE 153 AA; 17644 MW; 59F9980409964F84 CRC64;

Query Match 90.1%; Score 137; DB 2; Length 153;  
 Best Local Similarity 96.7%; Pred. No. 2.7e-12;  
 Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKTKTQLEHLLDLQMLINGINN 31  
 DB 21 ALTSSSTKTKTQLEHLLDLQMLINGINN 50

RESULT 19  
 Q13169  
 ID Q13169 PRELIMINARY; PRT; 156 AA.  
 AC Q13169;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Interleukin 2.  
 GN Name=IL2;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Xu D., Wu Y., Chen J., Yu L., Zhong M., Hui Y., Qu H.;  
 RT "Expression of human IL-2 from gene transferred mouse melanoma cells  
 and its effect on the growth of mouse melanoma.";  
 RL Chin. J. Microbiol. Immunol. 13:78-82(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Xu L.;  
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U25676; AAA70092.1; -;  
 DR HSP; P60568; IIRL.  
 DR GO; GO:0005576; C:extracellular; TAS.  
 DR GO; GO:0005134; F:interleukin-2 receptor binding; TAS.  
 DR GO; GO:0019209; P:kinase activator activity; TAS.  
 DR GO; GO:0006956; P:anti-apoptosis; TAS.  
 DR GO; GO:0007267; P:cell-cell signaling; TAS.  
 DR GO; GO:0006955; P:immune response; TAS.  
 DR GO; GO:0030101; P:natural killer cell activation; TAS.  
 DR GO; GO:0030307; P:positive regulation of cell growth; TAS.  
 DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.  
 DR GO; GO:0030217; P:T-cell differentiation; TAS.  
 DR InterPro; IPRO00979; 4\_helix cytokine.  
 DR InterPro; IPRO00779; Interleukin-2.  
 DR Pfam; PF00715; IL2; 1.  
 DR PRINTS; PR00265; INTERLEUKIN2.  
 DR ProDom; PD003649; Interleukin-2; 1.  
 DR SMART; SM00189; IL2; 1.  
 DR PROSITE; PS00424; INTERLEUKIN 2; 1.  
 SQ SEQUENCE 156 AA; 18002 MW; 8E0452D43B336389 CRC64;

Query Match 89.1%; Score 135.5; DB 2; Length 156;  
 Best Local Similarity 90.9%; Pred. No. 4.7e-12;  
 Matches 30; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 2 APTSSSTKTKTQLEHLLDLQMLINGINN 31  
 DB 21 APTSSSTKTKTQLEHLLDLQMLINGINN 53

RESULT 20  
 Q16334  
 ID Q16334 PRELIMINARY; PRT; 139 AA.  
 AC Q16334;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE IL-2 protein (Fragment).  
 GN Name=IL-2;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.

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RX MEDLINE=952319150; PubMed=7722480;
RA Eizenberg O., Faber-Elman A., Lotan M., Schwartz M.;
RT "Interleukin-2 transcripts in human and rodent brains: possible
expression by astrocytes.";
RL J. Neurochem. 64:1928-1936(1995).
DR EMBL; S7835; AAD14264.1; -.
DR HSSP; P60568; IIRL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0003134; F:interleukin-2 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
FT NON TER 139 139
SQ SEQUENCE 139 AA; 15986 MW; 731FBA406D0C63C5 CRC64;

Query Match 88.2%; Score 134; DB 2; Length 139;
Best Local Similarity 93.3%; Pred. NO. 6.9e-12;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 APTSSSTKTQLQLEHLLDLQWLINGINN 31
DB 17 APTSSSTKTQLXLEHLLDLQWLXGINN 46

RESULT 21
IL2_MIRAN
ID IL2_MIRAN STANDARD; PRT; 154 AA.
AC O62641;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN Name=IL2;
OS Mirounga angustirostris (Northern elephant seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Mirounga.
OX NCBI_TaxID=9716;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98136706; PubMed=9476229;
RA Shoda L.K.W., Brown W.C., Rice-Ficht A.C.;
RT "Sequence and characterization of phocine interleukin 2.";
RL J. Wildl. Dis. 34:81-90(1998).
CC -!- FUNCTION: Produced by T-cells in response to antigenic or
mitogenic stimulation, this protein is required for T-cell
proliferation and other activities crucial to regulation of the
immune response. Can stimulate B cells, monocytes, lymphokine-
activated killer cells, natural killer cells, and glioma cells (By
similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-2 family.
CC -----
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CC -----
DR EMBL; U79187; AAC12258.1; -.
DR HSSP; P01585; 1M49.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.

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DR PROSITE; PS00424; INTERLEUKIN_2; 1.
KW Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
KW T-cell.
FT SIGNAL 1 20 By similarity.
FT CHAIN 21 154 Interleukin-2.
FT CARBOHYD 23 23 O-linked (GalNAc..) (By similarity).
FT DISULFID 78 126 By similarity.
SQ SEQUENCE 154 AA; 17661 MW; 0C923337A4B16B6B CRC64;

Query Match 76.3%; Score 116; DB 1; Length 154;
Best Local Similarity 73.3%; Pred. NO. 3.9e-09;
Matches 22; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 2 APTSSSTKTQLQLEHLLDLQWLINGINN 31
DB 21 APTTSTTKTQQLEQLLDLRLINGVNN 50

RESULT 22
IL2_FELCA
ID IL2_FELCA STANDARD; PRT; 154 AA.
AC Q07885;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN Name=IL2;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93356765; PubMed=8352761;
RA Cozzi P.J., Padrid P.A., Takeda J., Alegre M.-A., Yuhki N., Leff A.R.;
RT "Sequence and functional characterization of feline interleukin 2.";
RL Biochem. Biophys. Res. Commun. 194:1038-1043(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Litman R., Gibbs C., Good R.A., Day N.K.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Produced by T-cells in response to antigenic or
mitogenic stimulation, this protein is required for T-cell
proliferation and other activities crucial to regulation of the
immune response. Can stimulate B cells, monocytes, lymphokine-
activated killer cells, natural killer cells, and glioma cells.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-2 family.
CC -----
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CC -----
DR EMBL; L19402; AAA02865.1; -.
DR EMBL; L25408; AAA51431.1; -.
DR PIR; JN0698; JN0698.
DR HSSP; P01585; 1M49.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
KW Cytokine; Glycoprotein; Growth factor; Immune response; Signal;
KW T-cell.
FT SIGNAL 1 20 By similarity.
FT CHAIN 21 154 Interleukin-2.
FT DISULFID 78 126 By similarity.

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FT CARBOHYD 111 111 N-linked (GlcNAc...) (Potential).
FT CONFLICT 3 4 KI -> RM (in Ref. 2).
FT CONFLICT 150 150 F -> I (in Ref. 2).
SQ SEQUENCE 154 AA; 17653 MW; 2E71E3BD8B9665EF CRC64;

Query Match 75.0%; Score 114; DB 1; Length 154;
Best Local Similarity 73.3%; Pred. No. 7.7e-09;
Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQQLQLEHLLDLQMLNGINN 31
DB 21 APASSTKKTQQLQLEHLLDLRLNGVNN 50

RESULT 23
Q9XT83 PRELIMINARY; PRT; 155 AA.
AC Q9XT83;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interleukin 2.
OS Halichoerus grypus (Gray seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Halichoerus.
OX NCBI_TaxID=9711;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99221046; PubMed=10206205; DOI=10.1016/S0165-2427(99)00009-4;
RA St-Laurent G., Beliveau C., Archambault D.;
RT "Molecular cloning and phylogenetic analysis of beluga whale
RT (Delphinapterus leucas) and grey seal (Halichoerus grypus) interleukin
RT 2."
RL Vet. Immunol. Immunopathol. 67:385-394(1999).
DR EMBL; AF072871; AD40848.1; -.
DR HSSP; P60568; IIRL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005134; P:interleukin-2 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR000779; 4_helix_cytokine.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
FT NON_TER 1
FT NON_TER 66
SQ SEQUENCE 155 AA; 17860 MW; F18F49AC672241A CRC64;

Query Match 71.4%; Score 108.5; DB 2; Length 155;
Best Local Similarity 74.2%; Pred. No. 5.2e-08;
Matches 23; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 2 APTSSSTKKTQQLQLEHLLDLQMLNGINN 31
DB 21 APTSSSTKKTQQLQLEHLLDLRLNGVNN 51

RESULT 24
Q9BG74 PRELIMINARY; PRT; 66 AA.
AC Q9BG74;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interleukin 2 (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Blood;
RA Markus S., Groene A., Baumgaertner W.;

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RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF333117; AAK01437.1; -.
DR HSSP; P60568; IIRL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005134; P:interleukin-2 receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
FT NON_TER 1
FT NON_TER 66
SQ SEQUENCE 66 AA; 7389 MW; 22A893P79DA2AE47 CRC64;

Query Match 70.7%; Score 107.5; DB 2; Length 66;
Best Local Similarity 71.0%; Pred. No. 2.8e-08;
Matches 22; Conservative 6; Mismatches 2; Indels 1; Gaps 1;

QY 2 APTSSSTKKTQQLQLEHLLDLQMLNGINN 31
DB 14 APTSSSTKKTQQLQLEHLLDLRLNGVNN 44

RESULT 25
IL2 CANFA
ID IL2 CANFA STANDARD; PRT; 155 AA.
AC Q29416; Q28249;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN Name=IL2;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=XRED21/12/93; TISSUE=Lymph node;
RX MEDLINE=95337423; PubMed=7612930;
RA Dunham S.P., Argyle D.J., Onions D.E.;
RT "The isolation and sequence of canine interleukin-2."
RL DNA Seq. 5:177-180(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96016696; PubMed=8571541; DOI=10.1016/0165-2427(94)05400-M;
RA Somborg R.L., Pullen R.P., Casal M.L., Patterson D.F., Felsburg P.J.,
RA Henthorn P.S.;
RT "A single nucleotide insertion in the canine interleukin-2 receptor
RT gamma chain results in X-linked severe combined immunodeficiency
RT disease."
RL Vet. Immunol. Immunopathol. 47:203-213(1995).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=Beagle; TISSUE=Spleen;
RX MEDLINE=95347614; PubMed=7622066; DOI=10.1016/0378-1119(95)00078-K;
RA Knapp D.W., Williams J.S., Andrisani O.M.;
RT "Cloning of the canine interleukin-2-encoding cDNA."
RL Gene 159:281-282(1995).
CC -!- FUNCTION: Produced by T-cells in response to antigenic or
CC mitogenic stimulation, this protein is required for T-cell
CC proliferation and other activities crucial to regulation of the
CC immune response. Can stimulate B cells, monocytes, lymphokine-
CC activated killer cells, natural killer cells, and glioma cells.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-2 family.
CC -----
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DR GO:0005134; F:interleukin-2 receptor binding; IEA.  
 DR GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR009079; 4\_helix\_cytokine.  
 DR InterPro; IPR000779; Interleukin-2.  
 DR Pfam; PF00715; IL2; 1.  
 DR PRINTS; PR00265; INTERLEUKIN2.  
 DR ProDom; PD003649; Interleukin-2; 1.  
 DR SMART; SM00189; IL2; 1.  
 DR PROSITE; PS00424; INTERLEUKIN\_2; 1.  
 FT NON\_TER 1  
 FT NON\_TER 138  
 SQ SEQUENCE 138 AA; 15739 MW; 351032995B670779 CRC64;

Query Match 67.8%; Score 103; DB 2; Length 138;  
 Best Local Similarity 73.3%; Pred. No. 3e-07;  
 Matches 22; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLLLDLQMLNGINN 31  
 DB 14 APTSSSKKETQHLEQLLLDLQELKGINN 43

## RESULT 32

ID IL2 RAT STANDARD; PRT; 155 AA.  
 AC P17108;  
 DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).  
 GN Name=IL2; Synonyms=IL-2;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89339608; PubMed=2788130;  
 RA McKnight A.J., Mason D.W., Barclay A.N.;  
 RT "Sequence of rat interleukin 2 and anomalous binding of a mouse  
 interleukin 2 cDNA probe to rat MHC class II-associated invariant  
 chain mRNA."  
 RL Immunogenetics 30:145-147 (1989).  
 CC -!- FUNCTION: Produced by T-cells in response to antigenic or  
 mitogenic stimulation, this protein is required for T-cell  
 proliferation and other activities crucial to regulation of the  
 immune response. Can stimulate B cells, monocytes, lymphokine-  
 activated killer cells, natural killer cells, and glioma cells.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the IL-2 family.

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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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EMBL; M22899; AAA41427.1; -.  
 DR PIR; A45882; A31278.  
 DR HSSP; P01585; IM49.  
 DR RGD; 620047; IL2.  
 DR InterPro; IPR009079; 4\_helix\_cytokine.  
 DR InterPro; IPR000779; Interleukin-2.  
 DR Pfam; PF00715; IL2; 1.  
 DR PRINTS; PR00265; INTERLEUKIN2.  
 DR ProDom; PD003649; Interleukin-2; 1.  
 DR SMART; SM00189; IL2; 1.  
 DR PROSITE; PS00424; INTERLEUKIN\_2; 1.  
 KW Cytokine; Glycoprotein; Growth factor; Immune response; Signal;  
 T-cell.  
 KW SIGNAL 1 20 By similarity.

FT CHAIN 21 155 Interleukin-2.  
 FT CARBOHYD 23 23 O-linked (GalNAc. .) (By similarity).  
 FT DISULFID 78 126 By similarity.  
 SQ SEQUENCE 155 AA; 17632 MW; 67A8554A73BF30A0 CRC64;  
 Query Match 63.8%; Score 97; DB 1; Length 155;  
 Best Local Similarity 66.7%; Pred. No. 2.8e-06;  
 Matches 20; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
 QY 2 APTSSSTKKTQLQLEHLLLDLQMLNGINN 31  
 DB 21 APTSSPAKETQHLEQLLLDLQVLLRGIDN 50

## RESULT 33

IL2 PIG STANDARD; PRT; 154 AA.  
 ID IL2 PIG  
 AC P26891;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).  
 GN Name=IL2;  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=T-cell;  
 RX MEDLINE=91274360; PubMed=2054386; DOI=10.1016/0167-4781(91)90019-I;  
 RA Goodall J.C., Emery D.C., Bailey M., English L.S., Hall L.;  
 RT "cDNA cloning of porcine interleukin 2 by polymerase chain reaction."  
 RL Biochim. Biophys. Acta 1089:257-258 (1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=T-cell;  
 RA Lefevre F.;  
 RL Submitted (MAY-1991) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Iwata H., Hasegawa A., Yamamoto M., Oida T., Endo Y., Inoue T.;  
 RT "Structure of the porcine chromosomal interleukin-2 gene."  
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Produced by T-cells in response to antigenic or  
 mitogenic stimulation, this protein is required for T-cell  
 proliferation and other activities crucial to regulation of the  
 immune response. Can stimulate B cells, monocytes, lymphokine-  
 activated killer cells, natural killer cells, and glioma cells.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the IL-2 family.

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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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EMBL; X56750; CAA40071.1; -.  
 DR EMBL; X58428; CAA41330.1; -.  
 DR EMBL; AB041935; BAB16110.1; -.  
 DR PIR; S16241; S16241.  
 DR HSSP; P01585; IM49.  
 DR InterPro; IPR009079; 4\_helix\_cytokine.  
 DR InterPro; IPR000779; Interleukin-2.  
 DR Pfam; PF00715; IL2; 1.  
 DR PRINTS; PR00265; INTERLEUKIN2.  
 DR ProDom; PD003649; Interleukin-2; 1.  
 DR SMART; SM00189; IL2; 1.  
 DR PROSITE; PS00424; INTERLEUKIN\_2; 1.  
 KW Cytokine; Glycoprotein; Growth factor; Immune response; Signal;

KW T-cell.  
 FT SIGNAL 1 20 By similarity.  
 FT CHAIN 21 154 Interleukin-2.  
 FT CARBOHYD 23 23 O-linked (GalNAc... ) (By similarity).  
 FT DISULFID 78 126 By similarity.  
 SQ SEQUENCE 154 AA; 17401 MW; F3B95E43DA3D3E1 CRC64;

Query Match 63.2%; Score 96; DB 1; Length 154;  
 Best Local Similarity 66.7%; Pred. No. 3.9e-06;  
 Matches 20; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 APTSSSTKTQLEHLLDLQMLINGINN 31  
 DB 21 APTSSSTKTQLEHLLDLQMLINGINN 50

RESULT 34  
 IL2\_MERUN STANDARD; PRT; 155 AA.  
 AC Q08081;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).  
 GN Name=IL2;  
 OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;  
 OC Meriones.  
 OX NCBI\_TaxID=10047;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=94174702; PubMed=8128610; DOI=10.1016/0165-2427(94)90015-9;  
 RA Mai Z., Kousoulas K.G., Horohov D.W., Klei T.R.;  
 RT "Cross-species PCR cloning of gerbil (Meriones unguiculatus) interleukin-2 cDNA and its expression in COS-7 cells.";  
 RL Vet. Immunol. Immunopathol. 40:63-71(1994).  
 CC -!- FUNCTION: Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B cells, monocytes, lymphokine-activated killer cells, natural killer cells, and glioma cells.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the IL-2 family.

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DR EMBL; X68779; CAA48679.1; -;  
 DR PIR; S33509; S33509.  
 DR HSP; P01585; IMA9.  
 DR InterPro; IPR009079; 4\_helix\_cytokine.  
 DR InterPro; IPR000779; Interleukin-2.  
 DR Pfam; PF00715; IL2; 1.  
 DR PRINTS; PR00265; INTERLEUKIN2.  
 DR ProDom; PD003649; Interleukin-2; 1.  
 DR SMART; SM00189; IL2; 1.  
 DR PROSITE; PS00424; INTERLEUKIN\_2; 1.  
 DR Cytokine; Glycoprotein; Growth factor; Immune response; Signal;  
 KW T-cell.  
 FT SIGNAL 1 20 By similarity.  
 FT CHAIN 21 155 Interleukin-2.  
 FT CARBOHYD 23 23 O-linked (GalNAc... ) (By similarity).  
 FT DISULFID 78 126 By similarity.  
 SQ SEQUENCE 155 AA; 17602 MW; D0F74AA1A381CDDA CRC64;

Query Match 62.5%; Score 95; DB 1; Length 155;

Best Local Similarity 66.7%; Pred. No. 5.5e-06;  
 Matches 20; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 APTSSSTKTQLEHLLDLQMLINGINN 31  
 DB 21 APTSSPAKEAQQLLEQLLDLQQLLRGINN 50

RESULT 35  
 Q865X2 PRELIMINARY; PRT; 154 AA.  
 AC Q865X2;  
 DT 01-JUN-2003 (Tremblrel. 24, Created)  
 DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)  
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 DE Interleukin 2.  
 GN Name=IL-2;  
 OS Lama glama (Llama).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.  
 OX NCBI\_TaxID=9844;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Raadan O., Lee S.-., Yoshida R., Chang K.-., Ohashi K., Sugimoto C., Onuma M.;  
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB107651; BAC75388.1; -;  
 DR HSP; F60568; IIRL.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005134; F:interleukin-2 receptor binding; IEA.  
 DR GO; GO:0006955; P:immune response; IEA.  
 DR InterPro; IPR009079; 4\_helix\_cytokine.  
 DR InterPro; IPR000779; Interleukin-2.  
 DR Pfam; PF00715; IL2; 1.  
 DR PRINTS; PR00265; INTERLEUKIN2.  
 DR ProDom; PD003649; Interleukin-2; 1.  
 DR SMART; SM00189; IL2; 1.  
 DR PROSITE; PS00424; INTERLEUKIN\_2; 1.  
 SQ SEQUENCE 154 AA; 17652 MW; 8020EC8DBB7BBA38 CRC64;

Query Match 61.2%; Score 93; DB 2; Length 154;  
 Best Local Similarity 66.7%; Pred. No. 1.1e-05;  
 Matches 20; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 APTSSSTKTQLEHLLDLQMLINGINN 31  
 DB 21 APTLSSTKDTKKQLEPLLDLQFLLRKVN 50

RESULT 36  
 IL2\_HORSE STANDARD; PRT; 149 AA.  
 AC P37997;  
 DT 01-OCT-1994 (Rel. 30, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).  
 GN Name=IL2;  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94160538; PubMed=8116217; DOI=10.1016/0165-2427(93)90070-K;  
 RA Vandergriff E.V., Horohov D.W.;  
 RT "Molecular cloning and expression of equine interleukin 2.";  
 RL Vet. Immunol. Immunopathol. 39:395-406(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Tavernor A.S., Allen W.R., Butcher G.W.;  
 RL Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: Produced by T-cells in response to antigenic or

```

Best Local Similarity   90.5%;   Pred. No. 2.6e-06;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 TSSSTKTKTQLQHLLHLLDLQM 24
        ||| ||||| ||||| |||||
Db       3 TSXSTKTKTQLQHLLHLLDLQM 23

RESULT 38
IL2 ORCOR IL2 ORCOR STANDARD; PRT; 152 AA.
AC O97513;
ID 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGFP)
DE (Fragment).
DE DE Name=IL2;
OS Orcinus orca (Killer whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Orcinus.
NCBI_TaxID=9733;
[1]
RN SEQUENCE FROM N.A.
RP Ness T.L., Bradley W.G., Reynolds J.E. III, Roess W.B.;
RT "Isolation and expression of the interleukin-2 gene from the killer
RL whale, Orcinus orca.";
RL Mar. Mamm. Sci. 14:531-543(1998).
CC -!- FUNCTION: Produced by T-cells in response to antigenic or
CC mitogenic stimulation, this protein is required for T-cell
CC proliferation and other activities crucial to regulation of the
CC immune response. Can stimulate B cells, monocytes, lymphokine-
CC activated killer cells, natural killer cells, and glioma cells (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the IL-2 family.
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CC EMBL; AF009570; AAD01426.1; -.
CC HSPF; P01585; IM49.
CC InterPro; IPR009079; 4_helix_cytokine.
CC InterPro; IPR000779; Interleukin-2.
CC pfam; PF00715; IL2; 1.
CC PRINTS; PR00265; INTERLEUKIN2.
CC ProDom; PD003649; Interleukin-2; 1.
CC SMART; SM00189; IL2; 1.
CC PROSITE; PS00424; INTERLEUKIN_2; 1.
CC KWC Ytceln; Glycoprotein; Growth factor; Immune response; Signal;
CC T-cell.
CC SIGNAL 1 20 By similarity.
CC CHAIN 21 >152 Interleukin-2.
CC CARBOHYD 23 23 O-linked (GalNAc.. .) (By similarity).
CC DISULFID 78 126 By similarity.
CC FT NON TER 152 152
SQ SEQUENCE 152 AA; 17424 MW; 308F91821ECCB764 CRC64;

Query Match 57.9%; Score 88; DB 1; Length 152;
Best Local Similarity 60.0%; Pred. No. 6e-05;
Matches 18; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY      2 APTSSSTKTKTQLQHLLHLLDLQMLNGINN 31
Db     21 APTSSSTNTKKVQSLLLOLDLQMLKEINN 50

```

## RESULT 39

Q71V48  
ID Q71V48 PRELIMINARY; PRT; 38 AA.  
AC Q71V48;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Interleukin-2 (Fragment).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Turner D.M., Sinnott P.J., Hutchinson I.V.;  
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF031845; AAB86861.1; -;  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005134; F:interleukin-2 receptor binding; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR000779; Interleukin-2.  
DR Pfam; PF0715; IL2; 1.  
DR ProDom; PD003649; Interleukin-2; 1.  
FT NON\_TER 38 38  
SQ SEQUENCE 38 AA; 4192 MW; 8DE4AE5344C2CBA3 CRC64;

Query Match 57.2%; Score 87; DB 2; Length 38;  
Best Local Similarity 100.0%; Pred. No. 1.8e-05;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLL 19  
DB 21 APTSSSTKKTQLQLEHLL 38  
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## RESULT 40

Q9XT84  
ID Q9XT84 PRELIMINARY; PRT; 154 AA.  
AC Q9XT84;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Interleukin 2.  
OS Delphinapterus leucas (Beluga whale).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;  
OC Monodontidae; Delphinapterus.  
OX NCBI\_TaxID=9749;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99221046; PubMed=10206205; DOI=10.1016/S0165-2427(99)00009-4;  
RA St-Laurent G., Beliveau C., Archambault D.;  
RT "Molecular cloning and phylogenetic analysis of beluga whale  
RT (Delphinapterus leucas) and grey seal (Halichoerus grypus) interleukin  
RT 2.";  
RL Vet. Immunol. Immunopathol. 67:385-394(1999).  
DR EMBL; AF072870; AAD40847.1; -;  
DR HSP; P60568; IIRL.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005134; F:interleukin-2 receptor binding; IEA.  
DR GO; GO:0006955; P:immune response; IEA.  
DR InterPro; IPR009079; 4\_helix\_cytokine.  
DR InterPro; IPR000779; Interleukin-2.  
DR Pfam; PF0715; IL2; 1.  
DR PRINTS; PR00265; INTERLEUKIN2.  
DR ProDom; PD003649; Interleukin-2; 1.  
DR SMART; SM00189; IL2; 1.  
DR PROSITE; PS00424; INTERLEUKIN 2; 1.  
SQ SEQUENCE 154 AA; 17652 MW; 4288D3D41D04F172 CRC64;

Query Match 54.6%; Score 83; DB 2; Length 154;  
Best Local Similarity 56.7%; Pred. No. 0.00034;  
Matches 17; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLLQLQILNGINN 31  
DB 21 APTSSSTENTKKQVQSLLQDLHLLKEINN 50  
|||||

Search completed: September 23, 2005, 12:48:03  
Job time : 55.8525 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 23, 2005, 12:40:19 ; Search time 24.3934 Seconds  
(without alignments)  
122.275 Million cell updates/sec

Title: US-10-727-514-2  
Perfect score: 152  
Sequence: 1 MPTSSSTKTKQLQLEHLLDLQMLNGINN 31

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : PIR 79:\*  
1: piri:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	147	96.7	153	1 ICHU2	interleukin-2 prec
2	147	96.7	153	1 ICHU2	interleukin-2 prec
3	114	75.0	154	2 JN0698	interleukin 2 prec
4	97	63.8	155	2 A31278	interleukin-2 prec
5	96	63.2	154	2 S16241	interleukin-2 prec
6	95	62.5	155	2 S33509	interleukin-2 - Mo
7	92	60.5	149	2 S31391	interleukin-2 prec
8	79	52.0	155	2 I45913	interleukin-2 prec
9	79	52.0	155	2 S38662	interleukin-2 - go
10	79	52.0	155	2 S11488	interleukin-2 prec
11	69	45.4	169	2 S37289	interleukin-2 prec
12	64	42.1	169	1 ICMS2	interleukin-2 prec
13	59.5	39.1	60	2 I68870	interleukin 2 - we
14	58.5	38.5	62	2 I54512	interleukin 2 - mo
15	57.5	37.8	72	2 I68871	interleukin 2 - mo
16	54	35.5	357	2 S12169	isopenicillin N ac
17	52	34.2	155	1 F64145	hypothetical prote
18	52	34.2	737	2 G82262	probable exopolysa
19	51	33.6	304	2 F95285	probable LysR-type
20	51	33.6	627	2 E70122	flagellar hook-asa
21	50	32.9	365	2 C70701	hypothetical prote
22	49	32.2	230	2 H82447	DNA-binding respon
23	49	32.2	543	2 S82217	methyl-accepting c
24	49	32.2	1130	2 A89130	protein F52E1.4 [i
25	48.5	31.9	240	2 T22210	hypothetical prote
26	48	31.6	189	2 H64307	hypothetical prote
27	48	31.6	441	2 AB1367	aminopeptidase C {
28	48	31.6	441	2 AB1736	aminopeptidase C {
29	48	31.6	595	2 JC8012	G protein-coupled

30	48	31.6	1061	1	GNLJG4	HIV-1 retropepsin
31	47.5	31.2	244	2	T11685	hypothetical prote
32	47.5	31.2	938	2	F86548	polymorphic outer
33	47.5	31.2	938	2	H72074	polymorphic membra
34	47	30.9	398	2	F80209	conserved hypothet
35	47	30.9	557	2	F89839	hypothetical prote
36	47	30.9	1008	2	T41244	SEC14 protein homo
37	47	30.9	1964	2	A59282	nonmuscle myosin I
38	46.5	30.6	159	2	T05656	hypothetical prote
39	46.5	30.6	211	2	C84888	hypothetical prote
40	46.5	30.6	466	2	E90228	amino acid specifi
41	46	30.3	293	2	A71946	hypothetical prote
42	46	30.3	323	2	H90434	hypothetical prote
43	46	30.3	380	1	C37760	galactokinase (EC
44	46	30.3	516	2	B64551	oligopeptide ABC t
45	46	30.3	571	2	H82355	peptide ABC transp
46	46	30.3	614	2	T18745	hypothetical prote
47	46	30.3	627	2	S46820	hypothetical prote
48	46	30.3	692	2	T32980	hypothetical prote
49	46	30.3	715	2	G86634	hypothetical prote
50	46	30.3	1403	2	S24548	homeotic protein p
51	46	30.3	1612	2	JC5210	DNA (cytosine-5)-
52	46	30.3	3724	2	T18427	hypothetical prote
53	45	29.6	307	2	T46103	hypothetical prote
54	45	29.6	325	2	F81159	DNA polymerase III
55	45	29.6	325	2	C81945	probable DNA-dirc
56	45	29.6	328	2	AC2415	hypothetical prote
57	45	29.6	333	2	S32114	85C protein - Myco
58	45	29.6	343	2	C89779	hypothetical prote
59	45	29.6	530	2	C82442	probable peptide A
60	45	29.6	715	2	B43943	ATP-dependent memb
61	45	29.6	752	2	D40899	pol polyprotein -
62	45	29.6	870	1	GNMVJA	pol polyprotein -
63	45	29.6	895	2	F75608	conserved hypothet
64	45	29.6	903	2	JE0327	dynam-in-related pr
65	45	29.6	903	2	T50334	dynam-in-related pr
66	45	29.6	1802	2	G71616	hypothetical prote
67	44.5	29.3	359	2	T22950	hypothetical prote
68	44.5	29.3	511	2	S44275	dopamine receptor
69	44.5	29.3	741	2	A45771	2-5A-dependent RNA
70	44	28.9	269	2	G91169	probable acyltrans
71	44	28.9	273	2	G86015	hypothetical prote
72	44	28.9	283	2	B97167	flagellin family p
73	44	28.9	288	2	B89930	hypothetical prote
74	44	28.9	324	2	A97036	probable membrane
75	44	28.9	347	2	A12010	two-component hybr
76	44	28.9	357	2	S23526	cinnamyl-alcohol d
77	44	28.9	357	2	S23525	cinnamyl-alcohol d
78	44	28.9	365	2	JC7527	nuclear retroviral
79	44	28.9	368	2	T46607	3-isopropylmalate
80	44	28.9	415	2	B85436	hypothetical prote
81	44	28.9	474	2	B69494	phenylalanyl-tRNA
82	44	28.9	487	2	A11146	hypothetical cell
83	44	28.9	581	2	S09140	coli intron protei
84	44	28.9	585	2	T19814	hypothetical prote
85	44	28.9	594	2	A86309	F20P23.3 protein -
86	44	28.9	628	2	B91145	probable integral
87	44	28.9	628	2	F85991	probable integral
88	44	28.9	943	2	S44636	I22b7.5 protein -
89	44	28.9	1019	2	T11560	pol polyprotein -
90	44	28.9	1034	2	D85119	acriflavin resista
91	44	28.9	1050	2	AE0380	multidrug efflux p
92	44	28.9	1182	2	T30189	myelin transcripti
93	44	28.9	1187	2	T46637	transcription fact
94	44	28.9	1188	2	T46608	zinc finger protei
95	44	28.9	1208	2	AE1947	chromosome segrega
96	44	28.9	1245	2	E83110	exodeoxyribonucle
97	44	28.9	1352	2	G84473	hypothetical prote
98	44	28.9	1482	2	S13495	pregnancy zone pro
99	43.5	28.6	115	2	D97846	hypothetical prote
100	43.5	28.6	200	2	F84080	hypothetical prote

## ALIGNMENTS

## RESULT 1

ICG12

Interleukin-2 precursor - common gibbon  
 N:Alternate names: IL-2; T-cell growth factor  
 C:Species: Hylobates lar [common gibbon, white-handed gibbon]  
 C>Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004  
 C:Accession: A94067; A01849  
 R:Chen, S.J.; Holbrook, N.J.; Mitchell, K.F.; Vallone, C.A.; Greengard, J.S.; Crabtree, Proc. Natl. Acad. Sci. U.S.A. 82, 7284-7288, 1985  
 A>Title: A viral long terminal repeat in the interleukin 2 gene of a cell line that contains a 5' LTR into the 3' noncoding region  
 A:Reference number: A94067; UID:86042650; PMID:3877307  
 A:Accession: A94067  
 A:Molecule type: mRNA  
 A:Residues: 1-153 <CH>  
 A:Cross-references: UNIPROT:P60569; GB:M11144; NID:G177014; PIDN:AAA35454.1; PID:G177015  
 A:Experimental source: leukemia cell line M1A 144; ATCC TIB 201  
 A>Note: the integration of a retrovirus sequence containing a 5' LTR into the 3' noncoding region  
 C:Superfamily: Interleukin-2  
 C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-153/Product: interleukin-2 #status predicted <IL2>  
 F:23/Binding site: carbohydrate (Thr) (covalent) #status predicted  
 F:78-125/Disulfide bonds: #status predicted

Query Match 96.7%; Score 147; DB 1; Length 153;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-14;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

2 APTSSSTKTKTQLEHLLDLQMLNGINN 31

Db

21 APTSSSTKTKTQLEHLLDLQMLNGINN 50

## RESULT 2

ICHU2

Interleukin-2 precursor [validated] - human  
 N:Alternate names: IL-2; T-cell growth factor  
 C:Species: Homo sapiens (man)  
 C>Date: 11-Aug-1983 #sequence\_revision 11-Aug-1983 #text\_change 09-Jul-2004  
 R:Holbrook, N.J.; Lieber, M.; Crabtree, G.R. Nucleic Acids Res. 12, 5005-5013, 1984  
 A>Title: DNA sequence of the 5' flanking region of the human interleukin 2 gene: homologous to the 5' flanking region of the human interleukin 2 gene  
 A:Reference number: A93524; UID:84247353; PMID:6330695  
 A:Accession: A01849  
 A:Molecule type: DNA  
 A:Residues: 1-153 <HOL>  
 A:Cross-references: UNIPROT:P60568; GB:X00695; GB:X00200; GB:X00201; GB:X00202; NID:G337  
 R:Fujita, T.; Takaoka, C.; Matsui, H.; Taniguchi, T. Proc. Natl. Acad. Sci. U.S.A. 80, 7437-7441, 1983  
 A>Title: Structure of the human interleukin 2 gene  
 A:Reference number: A21192; UID:84170243; PMID:6324170  
 A:Accession: A21192  
 A:Molecule type: DNA  
 A:Residues: 1-153 <FUJ>  
 A:Cross-references: UNIPROT:P60569; NID:G186294; PIDN:AA48509.1; PID:G5729676  
 R:Holbrook, N.J.; Smith, K.A.; Fornace Jr., A.J.; Comeau, C.M.; Wiskocil, R.L.; Crabtree Proc. Natl. Acad. Sci. U.S.A. 81, 1634-1638, 1984  
 A>Title: T-cell growth factor: complete nucleotide sequence and organization of the gene  
 A:Reference number: A20961; UID:84170356; PMID:6608729  
 A:Accession: A20961  
 A:Molecule type: DNA  
 A:Residues: 1-153 <HO>  
 A:Cross-references: GB:K02056; NID:G186302; PIDN:AAA98792.1; PID:G386819  
 R:Laabi, Y.; Gras, M.P.; Carbonnel, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapis, EMBO J. 11, 3897-3904, 1992  
 A>Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16) translocation  
 A:Reference number: S31208; UID:93010984; PMID:1396583  
 A:Accession: S31209  
 A:Molecule type: mRNA  
 A>Note: mutation of Phe-42 to Ala reduced binding to the IL-2 receptor 5-10 fold without

A:Residues: 11-117 <LAA>  
 A:Cross-references: EMBL:Z14955  
 A>Note: This sequence is shown from the beginning of the fragment to the chromosomal break  
 R:Taniguchi, T.; Matsui, H.; Fujita, T.; Takaoka, C.; Kashima, N.; Yoshimoto, R.; Hamuro Nature 302, 305-310, 1983  
 A>Title: Structure and expression of a cloned cDNA for human interleukin-2.  
 A:Reference number: A93297; UID:83167472; PMID:6403867  
 A:Accession: A93297  
 A:Molecule type: mRNA  
 A:Residues: 1-153 <TAN>  
 A:Cross-references: GB:V00564; NID:G33780; PIDN:CAA23827.1; PID:G33781  
 A:Experimental source: leukemic T-cell line, Jurkat-111, cloned from Jurkat-FHCR  
 R:Maeda, S.; Nishino, N.; Obaru, K.; Mita, S.; Nomiya, H.; Shimada, K.; Fujimoto, K.; Biochem. Biophys. Res. Commun. 115, 1040-1047, 1983  
 A>Title: Cloning of interleukin 2 mRNAs from human tonsils.  
 A:Reference number: A90113; UID:84023840; PMID:6312994  
 A:Accession: A90113  
 A:Molecule type: mRNA  
 A:Residues: 1-153 <MA>  
 A:Cross-references: GB:J00264; NID:G186294; PIDN:AA48509.1; PID:G5729676  
 A:Experimental source: tonsillar mononuclear cells  
 R:Devos, R.; Plaetinck, G.; Cheroutre, H.; Simons, G.; Degraeve, W.; Tavernier, J.; Reman Nucleic Acids Res. 11, 4307-4323, 1983  
 A>Title: Molecular cloning of human interleukin 2 cDNA and its expression in Escherichia coli  
 A:Reference number: A93478; UID:83246551; PMID:6306584  
 A:Accession: A93478  
 A:Molecule type: mRNA  
 A:Residues: 1-153 <DEV>  
 A:Cross-references: GB:V00564; NID:G33780; PIDN:CAA23827.1; PID:G33781  
 A:Experimental source: splenocytes  
 R:Eisenberg, O.; Faber-Elman, A.; Lotan, M.; Schwartz, M. J. Neurochem. 64, 1928-1936, 1995  
 A>Title: Interleukin-2 transcripts in human and rodent brains: possible expression by as  
 A:Reference number: I56518; UID:95239150; PMID:7722480  
 A:Accession: I56518  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-152 <EIZ>  
 A:Cross-references: GB:S77834; NID:G999000  
 A:Accession: I73624  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 5-7, 'P', 9-17, 'P', 19-32, 'X', 34-45, 'X', 47-143 <RES>  
 A:Cross-references: GB:S77835; NID:G999001; PIDN:AA14264.1; PID:G4261964  
 R:Nishino, N.; Obaru, K.; Maeda, S.; Shimada, K.; Onoue, K. Biomed. Res. 6, 197-205, 1985  
 A>Title: Organization of the DNA regions flanking the human interleukin 2 gene.  
 A:Reference number: I52528  
 A:Accession: I52528  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-68 <RE2>  
 A:Cross-references: GB:M33199; NID:G186296; PIDN:AAA59139.1; PID:G553508  
 R:Siebenlist, U.; Durand, D.B.; Bressler, P.; Holbrook, N.J.; Norris, C.A.; Kamoun, M.; Mol. Cell. Biol. 6, 3042-3049, 1986  
 A>Title: Promoter region of interleukin-2 gene undergoes chromatin structure changes and  
 A:Reference number: I57603; UID:87064618; PMID:3491296  
 A:Accession: I57603  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-68 <RE3>  
 A:Cross-references: GB:M13879; NID:G186305; PIDN:AAA59141.1; PID:G553509  
 R:Weir, M.P.; Chaplin, M.A.; Wallace, D.M.; Dykes, C.W.; Hobden, A.N. Biochemistry 27, 6883-6892, 1988  
 A>Title: Structure-activity relationships of recombinant human interleukin 2.  
 A:Reference number: I52401; UID:89062420; PMID:3264184  
 A:Contents: recombinant IL-2 and mutants expressed in E. coli  
 A:Accession: I52401  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 'M', 21-153 <RE4>  
 A:Cross-references: GB:M22005; NID:G186300; PIDN:AAA59140.1; PID:G386818  
 A>Note: mutation of Phe-42 to Ala reduced binding to the IL-2 receptor 5-10 fold without

R;Robb, R.J.; Kutny, R.M.; Panico, M.; Morris, H.R.; Chowdhry, V.  
Proc. Natl. Acad. Sci. U.S.A. 81, 6486-6490, 1984  
A;Title: Amino acid sequence and post-translational modification of human interleukin 2.  
A;Reference number: A94009; MUID:85038540; PMID:6333564  
A;Accession: A94009  
A;Molecule type: protein  
A;Residues: 21-153 <ROB>  
A;Note: disulfide bonds and carbohydrate binding site were determined  
A;Note: heterogeneity in Jurkat-derived IL-2 is primarily due to differences in glycosyl  
n in lacking 21-Ala (Ft-IL2-A and Ft-IL2-B) and 22-Pro (Ft-IL2-B)  
R;Conrad, H.S.; Nintz, M.; Dittmar, K.E.J.; Lindenmaier, W.; Hoppe, J.; Hauser, H.  
J. Biol. Chem. 264, 17368-17373, 1989  
A;Title: Expression of human interleukin-2 in recombinant baby hamster kidney, Ltk-, and  
de.  
A;Reference number: A34463; MUID:90008901; PMID:2793860  
A;Accession: A34463  
A;Molecule type: protein  
A;Residues: 21-35 <CON>  
A;Note: the O-linked glycosylation site in recombinant material matched that from human  
R;Grabenhorst, E.; Hofer, B.; Nintz, M.; Jaeger, V.; Conrad, H.S.  
Eur. J. Biochem. 215, 189-197, 1993  
A;Title: Biochemistry and secretion of human interleukin 2 glycoproteins variants from B  
A;Reference number: S34052; MUID:93345493; PMID:8344280  
A;Contents: annotation; glycosylation of variant forms expressed in insect cells  
C;Genetics:  
A;Gene: GDB:IL2  
A;Cross-references: GDB:119344; OMIM:147680  
A;Map position: 4q26-q27  
A;Introns: 49/3; 69/3; 117/3  
C;Superfamily: interleukin-2  
C;Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-153/Product: interleukin-2 #status experimental <IL2>  
F;23/Binding site: carbohydrate (Thr) (covalent) #status experimental  
F;78-125/Disulfide bonds: #status experimental  
Query Match 96.7%; Score 147; DB 1; Length 153;  
Best Local Similarity 100.0%; Pred. No. 3.4e-14;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 APTSSSTKTQQLQLEHLLDLQMLINGINN 31  
DB 21 APTSSSTKTQQLQLEHLLDLQMLINGINN 50  
RESULT 3  
JN0698  
interleukin 2 precursor - cat  
C;Species: Felis silvestris catus (domestic cat)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004  
C;Accession: JN0698  
R;Cozzi, P.J.; Padrid, P.A.; Takeda, J.; Alegre, M.L.; Yuhki, N.; Leff, A.R.  
Biochem. Biophys. Res. Commun. 194, 1038-1043, 1993  
A;Title: Sequence and functional characterization of feline interleukin 2.  
A;Reference number: JN0698; MUID:93356765; PMID:8352761  
A;Accession: JN0698  
A;Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-154 <COZ>  
A;Cross-references: UNIPROT:Q07885; GB:U19402; NID:G304313; PIDN:AAA02865.1; PID:G304314  
C;Superfamily: interleukin-2  
C;Keywords: growth factor

Query Match 75.0%; Score 114; DB 2; Length 154;  
Best Local Similarity 73.3%; Pred. No. 2.4e-09;  
Matches 22; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
QY 2 APTSSSTKTQQLQLEHLLDLQMLINGINN 31  
DB 21 APASSSTKTQQLQLEHLLDLQMLINGINN 50  
RESULT 4

A31278  
interleukin-2 precursor - rat  
N;Alternate names: IL-2; T-cell growth factor  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 26-Apr-1989 #sequence\_revision 26-Apr-1989 #text\_change 09-Jul-2004  
C;Accession: A45882; A31278  
R;McKnight, A.J.; Mason, D.W.; Barclay, A.N.  
Immunogenetics 30, 145-147, 1989  
A;Title: Sequence of rat interleukin 2 and anomalous binding of a mouse interleukin 2 c  
A;Reference number: A45882; MUID:89339608; PMID:2788130  
A;Accession: A45882  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-155 <MC>  
A;Cross-references: UNIPROT:P17108; GB:M22899; NID:G204909; PIDN:AAA41427.1; PID:G204910  
C;Superfamily: interleukin-2  
C;Keywords: cytokine; glycoprotein; growth factor; immunoregulation; T-cell  
Query Match 63.8%; Score 97; DB 2; Length 155;  
Best Local Similarity 66.7%; Pred. No. 7.7e-07;  
Matches 20; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
QY 2 APTSSSTKTQQLQLEHLLDLQMLINGINN 31  
DB 21 APTSSPAKETQOHLQQLLLDLQVLLRGIDN 50  
RESULT 5  
S16241  
interleukin-2 precursor - pig  
N;Alternate names: IL-2; T-cell growth factor  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C;Accession: S16241; S15473  
R;Goodall, J.C.; Emery, D.C.; Bailey, M.; English, L.S.; Hall, L.  
Biochim. Biophys. Acta 1089, 257-258, 1991  
A;Title: cDNA cloning of porcine interleukin 2 by polymerase chain reaction.  
A;Reference number: S16241; MUID:91274360; PMID:2054386  
A;Accession: S16241  
A;Molecule type: mRNA  
A;Residues: 1-154 <GOO>  
A;Cross-references: UNIPROT:P26891; EMBL:X56750; NID:G1991; PIDN:CAA40071.1; PID:G1992  
R;Lefevre, F.  
submitted to the EMBL Data Library, March 1991  
A;Description: Molecular cloning of porcine interleukin 2 cDNA by the polymerase chain  
A;Reference number: S15473  
A;Accession: S15473  
A;Molecule type: mRNA  
A;Residues: 1-154 <LEF>  
A;Cross-references: EMBL:X58428; NID:G2068; PIDN:CAA41330.1; PID:G2069  
C;Superfamily: interleukin-2  
C;Keywords: cytokine; glycoprotein; growth factor; immunoregulation; T-cell  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-154/Product: interleukin-2 #status predicted <MAT>  
Query Match 63.2%; Score 96; DB 2; Length 154;  
Best Local Similarity 66.7%; Pred. No. 1.1e-06;  
Matches 20; Conservative 4; Mismatches 6; Indels 0; Gaps 0;  
QY 2 APTSSSTKTQQLQLEHLLDLQMLINGINN 31  
DB 21 APTSSSTKTQQLQLEHLLDLQMLINGINN 50  
RESULT 6  
S33509  
interleukin-2 - Mongolian jird  
C;Species: Meriones unguiculatus (Mongolian jird)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S33509  
R;Mai, Z.; Klei, T.; Horohov, D.  
submitted to the EMBL Data Library, October 1992  
A;Description: Cross-species PCR cloning of Jird (Meriones unguiculatus) interleukin-2

A;Reference number: S33509  
A;Accession: S33509  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-155 <MAL>  
A;Cross-references: UNIPROT:Q08081; EMBL:X68779; NID:g577588; PIDN:CAA48679.1; PID:g3116  
C;Superfamily: interleukin-2

Query Match 62.5%; Score 95; DB 2; Length 155;  
Best Local Similarity 66.7%; Pred. No. 1.5e-06;  
Matches 20; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQQLQLEHLLDLQMLINGINN 31  
||||| | : : : ||||| : |||  
Db 21 APTSSPAKAAQQLQQLLDLQQLLRGINN 50  
||||| | : : : ||||| : |||

RESULT 7  
S31391  
interleukin-2 precursor - horse  
C;Species: Equus caballus (domestic horse)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S31391  
R;Tavernor, A.S.; Butcher, G.W.  
submitted to the EMBL Data Library, November 1992  
A;Description: cDNA cloning of equine interleukin-2 by polymerase chain reaction.  
A;Reference number: S31391  
A;Accession: S31391  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-149 <TAV>  
A;Cross-references: UNIPROT:P37997; EMBL:X69393; NID:g1076; PIDN:CAA49190.1; PID:g1077  
C;Superfamily: interleukin-2

Query Match 60.5%; Score 92; DB 2; Length 149;  
Best Local Similarity 56.7%; Pred. No. 4e-06;  
Matches 17; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQQLQLEHLLDLQMLINGINN 31  
||||| | : : : ||||| : |||  
Db 21 APTSSSKRETQQLKQLQMLKLLLEGVNN 50  
||||| | : : : ||||| : |||

RESULT 8  
I45913  
interleukin-2 precursor - bovine  
C;Species: Bos primigenius taurus (cattle)  
C;Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 09-Jul-2004  
C;Accession: I45913; S21470; S20761  
R;Cerratti, D.P.; McKereghan, K.; Iarsen, A.; Cantrell, M.A.; Anderson, D.; Gillis, S.;  
Proc. Natl. Acad. Sci. U.S.A. 83, 3223-3227, 1986  
A;Title: Cloning, sequence, and expression of bovine interleukin 2.  
A;Reference number: I45913; MUID:86205869; PMID:3517854  
A;Accession: I45913  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-155 <CER>  
A;Cross-references: UNIPROT:P05016; GB:M12791; NID:g163204; PIDN:AAA30586.1; PID:g163205  
R;Anikeeva, N.N.; Vinogradova, T.V.; Votoshin, O.N.  
submitted to the EMBL Data Library, December 1989  
A;Reference number: S21470  
A;Accession: S21470  
A;Molecule type: DNA  
A;Residues: 1-22 <DNA>  
A;Cross-references: EMBL:X17201; NID:g452; PIDN:CAA35062.1; PID:g453  
C;Genetics:  
A;Gene: IL-2  
C;Superfamily: interleukin-2  
C;Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell

Query Match 52.0%; Score 79; DB 2; Length 155;  
Best Local Similarity 53.3%; Pred. No. 0.00034;  
Matches 16; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQQLQLEHLLDLQMLINGINN 31  
||||| | : : : ||||| : |||  
Db 21 APTSSSTGNTMKVKSLLLDLQLLEKVKN 50  
||||| | : : : ||||| : |||

RESULT 9  
S38662  
interleukin-2 - goat  
C;Species: Capra aegagrus hircus (domestic goat)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S38662  
R;Rimstad, E.  
submitted to the EMBL Data Library, November 1993  
A;Description: The molecular cloning and expression of caprine interleukin 2.  
A;Reference number: S38662  
A;Accession: S38662  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-155 <RIM>  
A;Cross-references: UNIPROT:P36835; EMBL:X76063; NID:g416002; PIDN:CAA53664.1; PID:g4160  
C;Superfamily: interleukin-2

Query Match 52.0%; Score 79; DB 2; Length 155;  
Best Local Similarity 53.3%; Pred. No. 0.00034;  
Matches 16; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQQLQLEHLLDLQMLINGINN 31  
||||| | : : : ||||| : |||  
Db 21 APTSSSTGNTMKVKSLLLDLQLLEKVKN 50  
||||| | : : : ||||| : |||

RESULT 10  
S11488  
interleukin-2 precursor - sheep  
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C;Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C;Accession: S11488; S13102; S15517  
R;Goodall, J.C.; Emery, D.C.; Perry, A.C.F.; English, L.S.; Hall, L.  
Nucleic Acids Res. 18, 5883, 1990  
A;Title: cDNA cloning of ovine interleukin 2 by PCR.  
A;Reference number: S11488; MUID:91016933; PMID:2216781  
A;Accession: S11488  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-155 <GOO>  
A;Cross-references: UNIPROT:P19114; EMBL:X53934; NID:g1281; PIDN:CAA37881.1; PID:g1282  
R;Seow, H.F.; Rothel, J.S.; Radford, A.J.; Wood, P.R.  
Nucleic Acids Res. 18, 7175, 1990  
A;Title: The molecular cloning of ovine interleukin 2 gene by the polymerase chain react  
A;Reference number: S13102; MUID:91088336; PMID:2263496  
A;Accession: S13102  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-5,'L',7-155 <SEO>  
A;Cross-references: EMBL:X55641; NID:g1810; PIDN:CAA39165.1; PID:g1811  
R;Bujdosó, R.; Williamson, M.L.; Sargan, D.R.; Hein, W.H.; McConnell, I.  
submitted to the EMBL Data Library, April 1991  
A;Reference number: S15517  
A;Accession: S15517  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 21-153 <BUJ>  
A;Cross-references: EMBL:X60148  
C;Superfamily: interleukin-2

Query Match 52.0%; Score 79; DB 2; Length 155;  
Best Local Similarity 53.3%; Pred. No. 0.00034;  
Matches 16; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQQLQLEHLLDLQMLINGINN 31  
||||| | : : : ||||| : |||  
Db 21 APTSSSTGNTMKVKSLLLDLQLLEKVKN 50  
||||| | : : : ||||| : |||





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RESULT 21
C70701
hypothetical protein Rv0029 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: C70701
F:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churruarin, C.; Harris, D.; Gordon, L.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: C70701
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-365 <CON>
A:Cross-references: UNIPROT:P71599; GB:Z80233; GB:AL123456; NID:g3261645; PIDN:CAB02414
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv0029

Query Match 32.9%; Score 50; DB 2; Length 365;
Best Local Similarity 40.0%; Pred. No. 16;
Matches 12; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

Qy 2 APTSSSTKKTQLQLEHLALLDLQWILNGINN 31
| |||: || ||| ||| |||:
Db 43 AELSSNTAETATLAELHAKDLHRIVGSAND 72

RESULT 22
H82447
DNA-binding repressor regulator Hcr0532 (strain H37RV)

```

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C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: H82447
R:Heidelberg, J.F.; Eissen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
Chadson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: AB2035; MUID:20406933; PMID:10952301
A:Accession: H82447
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-230 <HEI>
A:Cross-references: UNIPROT:O9KM56; GB:AE004384; GB:AE003853; NID:g9657936; PIDN:AAF9643
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VCA0532
A:Map position: 2
C:Superfamily: ompR protein; response regulator homology

Query Match 32.2%; Score 49; DB 2; Length 230;
Best Local Similarity 40.9%; Pred. No. 14;
Matches 9; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MAPTSSSTKKTQLQLEHLIIDL 22
Db 121 LAPSTSEVQTRFELGDLVLDL 142

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methyl-accepting chemotaxis protein VC1298 [imported] - *Vibrio cholerae* (strain N16961 s  
 F82217  
 C/Species: *Vibrio cholerae*  
 C/Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 09-Jul-2004  
 C/Accession: F82217  
 R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;  
 Chardonson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.  
 l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
 Nature 406. 477-483. 2000

A;Title: DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.  
A;Reference number: A82035; MUID:20406833; PMID:10952301  
A;Accession: F82217  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-543 <HEI>  
A;Cross-references: UNIPROT:Q9KSF8; GB:AE004209; GB:AE003852; NID:g9655779; PIDN:AAF9445  
A;Experimental source: serogroup O1; strain N16961; biotype El Tor  
C;Genetics:  
A;Gene: VC1298  
A;Map position: 1

Query Match 32.2%; Score 49; DB 2; Length 543;  
Best Local Similarity 37.5%; Pred. No. 36;  
Matches 9; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 4 TSSSTKKTQLQLEHLLLDLQMLIN 27  
::||:::|||||:|:|  
Db 506 SASREISIDLEHLSQQLSLLN 529

RESULT 24  
A9130  
protein F52E1.4 [imported] - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 24-May-2001  
C;Accession: A89130  
R;Anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology  
A;Reference number: A75000; MUID:99069613; PMID:9851916  
A;Note: see websites genome.wustli.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_ele  
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and  
A;Accession: A89130  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1130 <STO>  
A;Cross-references: GB:chr\_V; PIDN:AAB37038.1; PID:gl086805; GSPDB:GN00023; CESP:F52E1.4  
C;Genetics:  
A;Gene: F52E1.4  
A;Map position: 5  
C;Superfamily: membrane-bound guanylate cyclase; guanylate cyclase catalytic domain hom

Query Match 32.2%; Score 49; DB 2; Length 1130;  
Best Local Similarity 46.2%; Pred. No. 81;  
Matches 12; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 4 TSSSTKKTQLQLEHLLLDLQMLINGI 29  
:::|||||:|:|  
Db 906 TTLASKCTPLQVVNLLNDLYTFDGI 931

RESULT 25  
T22210  
hypothetical protein F44G4.7 - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T22210  
R;Sims, M.  
submitted to the EMBL Data Library, June 1995  
A;Reference number: Z19530  
A;Accession: T22210  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-240 <WIL>  
A;Cross-references: UNIPROT:Q20417; EMBL:Z49910; PIDN:CAA90123.1; GSPDB:GN00020; CESP:F4  
A;Experimental source: clone F44G4  
C;Genetics:  
A;Gene: CESP:F44G4.7  
A;Map position: 2  
A;Introns: 123/2; 159/3  
C;Superfamily: *Caenorhabditis elegans* hypothetical protein F44G4.7

Query Match 31.9%; Score 48.5; DB 2; Length 240;  
Best Local Similarity 44.0%; Pred. No. 17;  
Matches 11; Conservative 9; Mismatches 4; Indels 1; Gaps 1;

QY 3 PTSSSTKKTQLQLEHLLLDLQMLIN 27  
|||||:::|:|:|:|:|:|  
Db 146 PTSSQEQREKWRVK-LLIDLEMLIS 169

RESULT 26  
H64307  
hypothetical protein MJ0064 - *Methanococcus jannaschii*  
C;Species: *Methanococcus jannaschii*  
C;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 09-Jul-2004  
C;Accession: H64307  
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,  
; Reich, C.I.; Overbeek, R.; Kirkness, E.P.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;  
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.  
Science 273, 1058-1073, 1996  
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.  
A;Title: Complete genome sequence of the methanogenic archaeon, *Methanococcus jannaschii*  
A;Reference number: A64300; MUID:96337999; PMID:8688087  
A;Accession: H64307  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-189 <BUL>  
A;Cross-references: UNIPROT:Q60376; GB:U67464; GB:L77117; NID:gl590852; PIDN:AAB98051.1;  
C;Genetics:  
A;Map position: FOR61888-62457  
A;Start codon: GTG

Query Match 31.6%; Score 48; DB 2; Length 189;  
Best Local Similarity 32.1%; Pred. No. 15;  
Matches 9; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 4 TSSSTKKTQLQLEHLLLDLQMLINGIN 31  
:|||||:|:|:|:|:|:|  
Db 22 SSSSVLETEIVLDEIITKLNLISEINN 49

RESULT 27  
AB1367  
aminopeptidase C [imported] - *Listeria monocytogenes* (strain EGD-e)  
C;Species: *Listeria monocytogenes*  
C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 09-Jul-2004  
C;Accession: AB1367  
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker  
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.  
D.; Jones, L.M.; Karst, U.  
Science 294, 849-852, 2001  
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma  
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,  
A;Title: Comparative genomics of *Listeria species*.  
A;Reference number: AB1077; MUID:21537279; PMID:11679669  
A;Accession: AB1367  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-441 <GLA>  
A;Cross-references: UNIPROT:O69192; GB:NC\_003210; PIDN:CAD00416.1; PID:gl6411826; GSPDB:  
A;Experimental source: strain EGD-e  
C;Genetics:  
A;Gene: pepC  
C;Superfamily: aminopeptidase C (bleomycin hydrolase)

Query Match 31.6%; Score 48; DB 2; Length 441;  
Best Local Similarity 34.6%; Pred. No. 40;  
Matches 9; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 5 SSSTKKTQLQLEHLLLDLQMLINGIN 30  
::|||:|:|:|:|:|:|  
Db 344 TAMTKAERLDYKHSMLTHAMVLTGVN 369



A:Reference number: A30045; MUID:88232906; PMID:3374586  
A:Accession: B30045  
A:Molecule type: DNA  
A:Residues: 1-1061 <FUK>  
A:Cross-references: EMBL:X07805; NID:G61748; PID:gl335593  
C:Comment: Specific enzymatic cleavages may yield mature proteins including protease, r  
C:Genetics:  
A:Gene: pol  
A:Superfamily: pol polyprotein  
C:Keywords: aspartic proteinase; hydrolase; nucleotidyltransferase; polyprotein; reverse  
E:111-210/Product: retropepsin #status predicted <RTP>  
F:113/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 31.6%; Score 48; DB 1; Length 1061;  
Best Local Similarity 52.9%; Pred. No. 1.1e+02;  
Matches 9; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 11 TQLQLHLLDLQMLN 27  
DB 976 TQLEIQLQTKIQILN 992

RESULT 31

T11685  
Hypothetical protein SPBC21D10.13 SPBC1921.07c - fission yeast (Schizosaccharomyces pombe)  
C:Species: Schizosaccharomyces pombe  
C:Date: 16-Jul-1999 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C:Accession: T11685; T39791  
R:Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, September 1998  
A:Reference number: Z17313  
A:Accession: T11685  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-155 <SEE>  
A:Cross-references: UNIPROT:Q9USW9; EMBL:AL031536; NID:e1319499  
A:Experimental source: strain 972h(-)  
R:Seeger, K.; Harris, D.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.  
submitted to the EMBL Data Library, October 1999  
A:Reference number: Z21816  
A:Accession: T39791  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 129-244 <SE2>  
A:Cross-references: EMBL:AL122033; PIDN:CAB58973.1; GSPDB:GN00067; SPDB:SPBC1921.07c  
A:Map position: IIR  
A:Note: SPBC21D10.13  
A:Note: intron positions not resolved (incomplete sequence)

Query Match 31.2%; Score 47.5; DB 2; Length 244;  
Best Local Similarity 45.8%; Pred. No. 24;  
Matches 11; Conservative 4; Mismatches 6; Indels 3; Gaps 1;

QY 4 TSSSTKTKQLQLHLLDLQMLN 27  
DB 59 TSEKQK---ELEHTMQSLEMIIN 79

RESULT 32

F86548  
polymorphic outer membrane protein E family [imported] - Chlamydia pneumoniae (strain  
C:Species: Chlamydia pneumoniae; Chlamydia pneumoniae  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
C:Accession: F86548  
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is  
Nucleic Acids Res. 28, 2311-2314, 2000  
A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.  
A:Reference number: A86491; MUID:20330349; PMID:10871362  
A:Accession: F86548  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-938 <STO>



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C:Superfamily: Arabidopsis thaliana hypothetical protein F22I13.50

Query Match          30.6%;   Score 46.5;   DB 2;   Length 211;
Best Local Similarity 46.4%;   Pred. No. 29;
Matches 13; Conservative 3; Mismatches 9; Indels 3; Gaps 1;

QY      3 PTSSSTKTKTQLEHLLLDLQWLINGIN 30
      |||::||| | | | | | | | | | |
DB     117 PTPTSHK---LDWEERYLHQLMNLKLN 141

RESULT 40
E90228
amino acid specific permease [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: E90228
F:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.;
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.;
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: E90228
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-466 <KUR>
A:Cross-references: UNIPROT:Q9UKH3; GB:AE005641; NID:g13813962; PIDN:AAK41084.1
C:Genetics:
A:Gene: SSO0786

Query Match          30.6%;   Score 46.5;   DB 2;   Length 466;
Best Local Similarity 38.1%;   Pred. No. 70;
Matches 16; Conservative 5; Mismatches 10; Indels 11; Gaps 2;

QY      1 MAPTSSSTKKT---QLQLEHLLLDLQWLIN-----GINN 31
      |||::||| | | | | | | | | | |
DB     223 VASEAKVPKTLPKALLLEFLLGVGLINAYAQTVVYGVNN 264

Search completed: September 23, 2005, 12:48:58
Job time : 27.3934 secs

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